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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:07:51 ; Search time 4385.97 Seconds
(without alignments)
10964.406 Million cell updates/sec

Title: US-10-679-951-1
Perfect score: 846
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
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5: gb_ov:*
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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	846	100.0	846	6	AX663342	AX663342 Sequence
2	674	79.7	1008	6	AX663348	AX663348 Sequence
3	674	79.7	1008	11	AY893435	AY893435 Synthetic
4	674	79.7	1318	6	AX481417	AX481417 Sequence
5	674	79.7	1349	6	AR380630	AR380630 Sequence
6	674	79.7	1349	8	HUMMO3A	M83246 Human monoc
7	674	79.7	1353	8	BC002788	BC002788 Homo sapi
8	674	79.7	1363	6	AX787055	AX787055 Sequence
9	674	79.7	1363	8	HSUPARAA	X51675 H.sapiens u
10	674	79.7	1400	6	A18757	A18757 u-PA recept
11	674	79.7	1400	6	BD140440	BD140440 Urokinase
12	674	79.7	1400	6	BD188995	BD188995 Antibodie
13	674	79.7	1400	6	I21305	I21305 Sequence 12
14	674	79.7	1407	6	I08456	I08456 Sequence 8
15	674	79.7	1740	6	CQ870630	CQ870630 Sequence
16	674	79.7	1743	6	CS050233	CS050233 Sequence
17	674	79.7	1743	6	AR659305	AR659305 Sequence
18	674	79.7	1745	6	AR659486	AR659486 Sequence
19	674	79.7	1883	6	CQ492946	CQ492946 Sequence
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24	669.8	79.2	873	6	AX663346	AX663346 Sequence
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27	668.8	79.1	1008	11	AY892848	AY892848 Synthetic
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31	628.2	74.3	967	8	AF257789	AF257789 Homo sapi
32	626	74.0	1046	8	AF302072	AF302072 Cercopith
33	626	74.0	1067	8	AF302073	AF302073 Macaca fa
34	567.8	67.1	952	8	AY029180	AY029180 Homo sapi
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36	526	62.2	589	6	I08455	I08455 Sequence 6
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45	281.6	33.3	409	6	AX256054	AX256054 Sequence

ALIGNMENTS

RESULT 1
AX663342
LOCUS AX663342 846 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1 from Patent WO02082077.
ACCESSION AX663342
VERSION AX663342.1 GI:29163684
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
TITLE Production of polyclonal monospecific antibodies against upar variants del4, del5 and del4+5, and the use thereof for diagnostic and therapeutical purposes
JOURNAL Patent: WO 02082077-A 1 17-OCT-2002;
Wilex AG (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
CDS 1. .846
/note="unnamed protein product"
/codon_start=1
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ORIGIN

Query Match 100.0%; Score 846; DB 6; Length 846;
Best Local Similarity 100.0%; Pred. No. 8.9e-206;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        601 AACCAAAGCTATATGGTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTG 660
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Qy        721 CACCCAGACCTGGATGTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCAT 780
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Qy        841 ACCTAA 846
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Db        841 ACCTAA 846
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RESULT 2
AX663348
LOCUS AX663348 1008 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 7 from Patent WO02082077.
ACCESSION AX663348
VERSION AX663348.1 GI:29163690
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
TITLE Production of polyclonal monospecific antibodies against upar variants del4, del5 and del4+5, and the use thereof for diagnostic and therapeutical purposes
JOURNAL Patent: WO 02082077-A 7 17-OCT-2002;
Wilex AG (DE)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 79.7%; Score 674; DB 6; Length 1008;
Best Local Similarity 83.9%; Pred. No. 1.1e-161;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

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Db          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        310 ----------------------------------------------------GGGCGTCCA 318
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Qy        619 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 678
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LOCUS       AY893435               1008 bp    mRNA    linear   SYN 16-MAR-2005
DEFINITION  Synthetic construct Homo sapiens clone FLH127783.01X plasminogen
            activator urokinase receptor (PLAUR) mRNA, complete cds.
ACCESSION   AY893435
VERSION     AY893435.1  GI:60818642
KEYWORDS    Human ORF Project.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B.,
            Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
  TITLE     Cloning of human full-length CDS FLEXGene in
            Gateway(TM)recombinational vector system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B.,
            Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2005) Biological Chemistry and Molecular
            Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
            Cambridge, MA 02141, USA
COMMENT     This CDS clone is a part of a collection of human full-length
            expression clones generated by Harvard Institute of Proteomics.
            This ORF clone has been cloned with normalized stop-codon. AttB
            recombination sites have been added to either end of the ORF and
            directionally cloned using the Gateway cloning system into pDONR
            201. Additional sequences in the clone:  'ACC' before the 'ATG'
            (corresponding to ribosomal binding site and Kozak consensus
            sequences).  Each clone is clonally isolated and full-length
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     CDS             1. .1008
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ORIGIN
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  Query Match             79.7%;  Score 674;  DB 11;  Length 1008;
  Best Local Similarity   83.9%;  Pred. No. 1.1e-161;
  Matches  846;  Conservative    0;  Mismatches    0;  Indels  162;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy        499 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 558
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Db        661 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 720

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Qy        619 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 678
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Db        781 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 840
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Qy        679 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 738
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Db        901 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 960

Qy        799 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 846
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Db        961 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1008


RESULT 4
AX481417
LOCUS       AX481417               1318 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 31 from Patent WO02055693.
ACCESSION   AX481417
VERSION     AX481417.1  GI:22316331
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
  TITLE     Method for inhibiting the expression of a target gene
  JOURNAL   Patent: WO 02055693-A 31 18-JUL-2002;
            Ribopharma AG (DE)
FEATURES             Location/Qualifiers
     source          1. .1318
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             79.7%;  Score 674;  DB 6;  Length 1318;
  Best Local Similarity   83.9%;  Pred. No. 1.1e-161;
  Matches  846;  Conservative    0;  Mismatches    0;  Indels  162;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Db         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        310 ---------------------------------------------------------- 309

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Qy        319 AAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGCTGCCCGGGCTCCAATGGT 378
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Qy        439 GGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 498
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Qy        499 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 558
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Db        721 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 780

Qy        619 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 678
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Db        781 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 840

Qy        679 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 738
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Db        841 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 900

Qy        739 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 798
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Qy        799 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1008


RESULT 5
AR380630
LOCUS       AR380630               1349 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1175 from patent US 6607879.
ACCESSION   AR380630
VERSION     AR380630.1  GI:40088264
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1349)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1175 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .1349
                     /organism="unknown"
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ORIGIN

  Query Match             79.7%;  Score 674;  DB 6;  Length 1349;
  Best Local Similarity   83.9%;  Pred. No. 1.1e-161;
  Matches  846;  Conservative    0;  Mismatches    0;  Indels  162;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:05:06 ; Search time 519.437 Seconds
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Perfect score: 846
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 846

Scoring table: IDENTITY_NUC
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	674	79.7	1008	9	ABZ26099	Abz26099 Human uPA
3	674	79.7	1318	6	ABV78147	Abv78147 Human uro
4	674	79.7	1318	6	ABZ35723	Abz35723 Human UPA
5	674	79.7	1318	6	ABX09966	Abx09966 Human UPA
6	674	79.7	1318	6	ABL91688	Abl91688 Human pol
7	674	79.7	1349	11	ADI31849	Adi31849 Human cDN
8	674	79.7	1349	13	ADS83916	Ads83916 Human lym
9	674	79.7	1363	10	AAD56134	Aad56134 Human uro
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17	674	79.7	1407	2	AAT89675	Aat89675 Human pho
18	674	79.7	1548	14	ADZ80553	Adz80553 Plasminog
19	674	79.7	1740	13	ADR46626	Adr46626 Cancer-as
20	674	79.7	1743	8	ACC50260	Acc50260 Breast ca
21	674	79.7	1743	11	ADN39792	Adn39792 Cancer/an
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26	674	79.7	1743	13	ADP24413	Adp24413 PRO polyp
27	674	79.7	1743	14	AEB54689	Aeb54689 DNA encod
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33	669	79.1	1400	4	AAS12134	Aas12134 Human u-P
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35	653.2	77.2	1400	2	AAX19823	Aax19823 Urokinase
36	644	76.1	1370	8	ABX34691	Abx34691 Human mdd
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44	526	62.2	589	2	AAQ71650	Aaq71650 Human PIP
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ALIGNMENTS

RESULT 1
ABZ26096
ID ABZ26096 standard; cDNA; 846 BP.
XX
AC ABZ26096;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human uPAR exon 4 deletion variant encoding cDNA SEQ ID NO 1.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; gene; ss.
XX
OS Homo sapiens.
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FH Key Location/Qualifiers
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FT /product= "uPAR exon 4 deletion variant"
XX
PN DE10117381-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001DE-01017381.
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PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR P-PSDB; ABP60419.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 1; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a

```
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 4 deletion variant encoding cDNA
CC   of the invention
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  Best Local Similarity   100.0%;  Pred. No. 7.1e-217;
  Matches  846;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        361 TGCCCGGGCTCCAATGGTTTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAAC 420
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Db        361 TGCCCGGGCTCCAATGGTTTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAAC 420

Qy        421 ACCACCAAATGCAACGAGGGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGC 480
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Qy        781 CTCAGCCTCACCATCACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGG 840
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Db        781 CTCAGCCTCACCATCACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGG 840

Qy        841 ACCTAA 846
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Db        841 ACCTAA 846
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RESULT 2
ABZ26099
ID   ABZ26099 standard; cDNA; 1008 BP.
XX
AC   ABZ26099;
XX
DT   27-MAR-2003  (first entry)
XX
DE   Human uPAR encoding cDNA SEQ ID NO 7.
XX
KW   Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW   cancer; gene; ss.
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "uPAR"
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PN   DE10117381-A1.
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PD   10-OCT-2002.
XX
PF   06-APR-2001; 2001DE-01017381.
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PR   06-APR-2001; 2001DE-01017381.
XX
PA   (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI   Luther T,  Magdolen V,  Schmitt M,  Muehlenweg B;
XX
DR   WPI; 2003-168688/17.
DR   P-PSDB; ABP60422.
XX
PT   New nucleic acid encoding a deletion variant of a urokinase receptor
PT   which has one or two exons missing, is useful to detect and treat cancer,
PT   particularly breast and ovarian cancer.
XX
PS   Disclosure; Fig 4; 28pp; German.
XX
CC   The invention relates to a nucleic acid encoding a deletion variant of a
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a the wildtype uPAR encoding cDNA of the
CC   invention
XX
SQ   Sequence 1008 BP; 229 A; 306 C; 279 G; 194 T; 0 U; 0 Other;

  Query Match             79.7%;  Score 674;  DB 9;  Length 1008;
  Best Local Similarity   83.9%;  Pred. No. 1.2e-170;
  Matches  846;  Conservative    0;  Mismatches    0;  Indels  162;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Db          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:10:21 ; Search time 3423.34 Seconds
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Perfect score: 846
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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	674	79.7	1008	11	DQ050301	DQ050301 Homo sapi
	2	674	79.7	1303	4	CR606767	CR606767 full-leng
	3	674	79.7	1320	4	CR611518	CR611518 full-leng
	4	674	79.7	1348	4	CR591481	CR591481 full-leng
	5	669.2	79.1	1008	11	DQ050302	DQ050302 Pan trogl
	6	619	73.2	1724	4	CR601067	CR601067 full-leng
	7	599	70.8	1078	3	BM543893	BM543893 AGENCOURT
	8	572.8	67.7	954	1	AL556275	AL556275 AL556275
	9	561	66.3	1145	3	BM922342	BM922342 AGENCOURT
	10	560.8	66.3	1130	3	BM906800	BM906800 AGENCOURT
	11	556.4	65.8	983	1	AL554548	AL554548 AL554548
	12	533.8	63.1	905	3	BI906745	BI906745 603064474
	13	530	62.6	641	2	BE876180	BE876180 601485681
	14	529	62.5	560	6	CB158636	CB158636 K-EST0218
c	15	520.8	61.6	971	1	AL577205	AL577205 AL577205
c	16	512.8	60.6	944	1	AL577275	AL577275 AL577275
c	17	505.4	59.7	953	1	AL525210	AL525210 AL525210
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	19	493	58.3	539	1	AA455222	AA455222 zx79h09.r
	20	489.2	57.8	972	5	BU163129	BU163129 AGENCOURT
c	21	482	57.0	718	6	CD367492	CD367492 UI-H-FT1-
	22	482	57.0	841	8	DR760518	DR760518 HESC4_117
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	24	473.8	56.0	892	6	CA489863	CA489863 AGENCOURT
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	27	459.4	54.3	968	1	AL554495	AL554495 AL554495
	28	454	53.7	492	3	BI793227	BI793227 ie49e04.y
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	31	446.4	52.8	449	6	CB144030	CB144030 K-EST0198
	32	444.8	52.6	900	6	CA488827	CA488827 AGENCOURT
	33	440	52.0	1030	3	BM914922	BM914922 AGENCOURT
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	36	429.8	50.8	691	1	AL710258	AL710258 DKFZp686G
	37	428.4	50.6	811	7	CR975202	CR975202 CR975202
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	42	416	49.2	1064	3	BM903666	BM903666 AGENCOURT
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	44	410.4	48.5	586	1	AA443505	AA443505 zw34e01.r
c	45	409.2	48.4	765	5	BU634198	BU634198 UI-H-FL1-

ALIGNMENTS

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LOCUS DQ050301 1008 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens PLAUR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ050301
VERSION DQ050301.1 GI:66903500
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN

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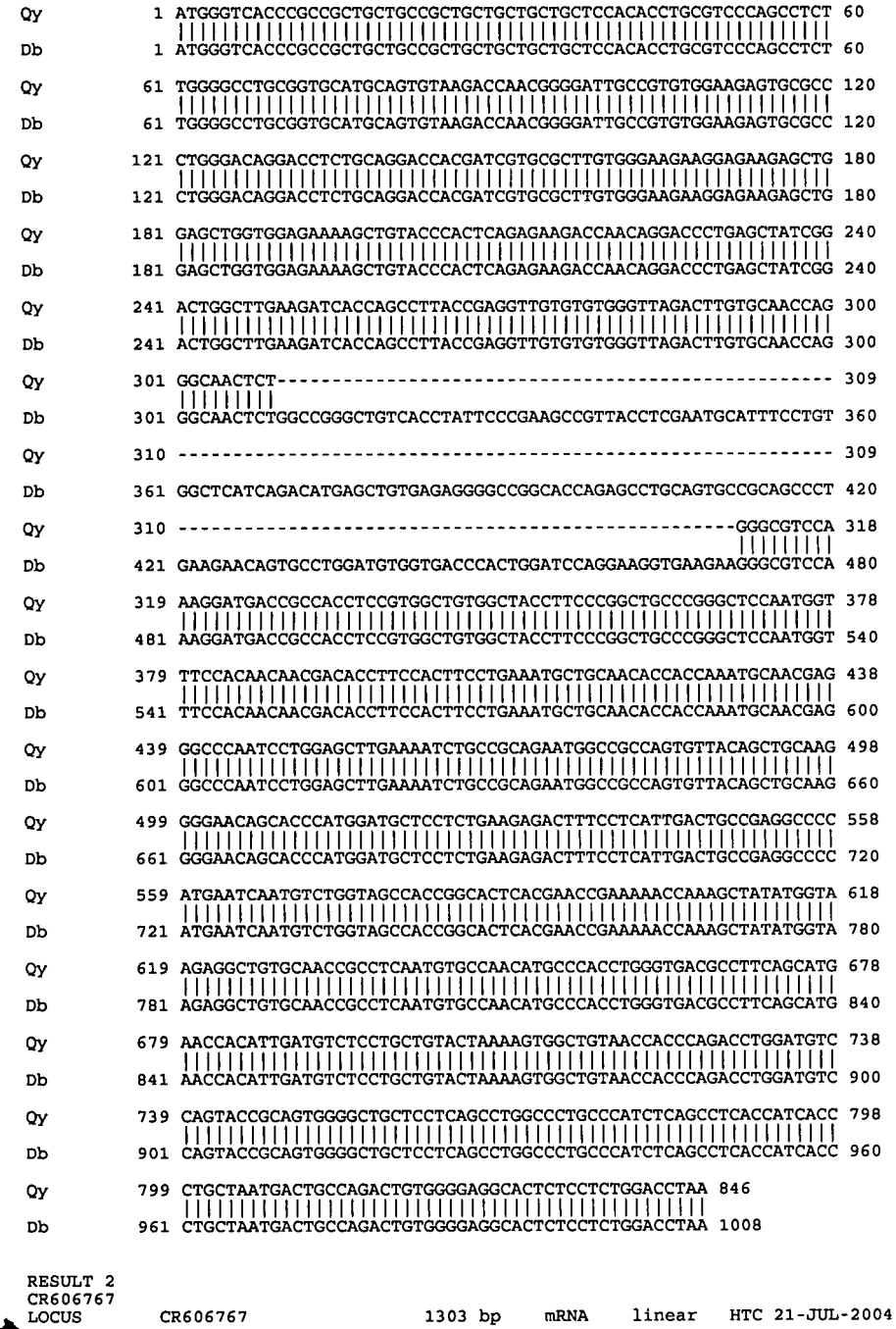
Best Local Similarity 83.9%; Pred. No. 1e-170;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;



RESULT 2
CR606767
LOCUS CR606767 1303 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DK001YE24 of HeLa cells Cot 25-normalized of Homo sapiens (human).
ACCESSION CR606767
VERSION CR606767.1 GI:50487574
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1303)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1303)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK001YE24"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

Query Match 79.7%; Score 674; DB 4; Length 1303;
Best Local Similarity 83.9%; Pred. No. 1.1e-170;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:24:01 ; Search time 171.289 Seconds
(without alignments)
8779.420 Million cell updates/sec

Title: US-10-679-951-1
Perfect score: 846
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	674	79.7	1349	3	US-09-023-655-1175	Sequence 1175, Ap
	2	674	79.7	1400	2	US-08-085-122-12	Sequence 12, Appl
	3	674	79.7	1400	3	US-08-442-108B-22	Sequence 22, Appl
	4	674	79.7	1743	3	US-09-949-002-60	Sequence 60, Appl
	5	674	79.7	1745	3	US-09-949-002-241	Sequence 241, App
	6	255	30.1	25966	3	US-09-949-002-632	Sequence 632, App
	7	255	30.1	25966	3	US-09-949-002-813	Sequence 813, App
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c	9	254.6	30.1	601	3	US-09-949-002-9335	Sequence 9335, Ap
c	10	144.6	17.1	601	3	US-09-949-002-2315	Sequence 2315, Ap
c	11	144.6	17.1	601	3	US-09-949-002-9331	Sequence 9331, Ap
c	12	139.8	16.5	601	3	US-09-949-002-2316	Sequence 2316, Ap
c	13	139.8	16.5	601	3	US-09-949-002-9332	Sequence 9332, Ap
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c	16	75	8.9	601	3	US-09-949-002-2307	Sequence 2307, Ap
c	17	75	8.9	601	3	US-09-949-002-9323	Sequence 9323, Ap
	18	59	7.0	76	3	US-09-313-294A-4742	Sequence 4742, Ap
	19	59	7.0	114	3	US-09-313-294A-5817	Sequence 5817, Ap
	20	50	5.9	50	3	US-10-131-827-2347	Sequence 2347, Ap
	21	43.6	5.2	1527	3	US-09-489-039A-716	Sequence 716, App
c	22	42	5.0	56	3	US-09-381-244B-24	Sequence 24, Appl
	23	39.8	4.7	2070	2	US-07-766-351-6	Sequence 6, Appli
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	26	39.8	4.7	2515	3	US-10-281-867-1	Sequence 1, Appli
	27	39.8	4.7	2515	3	US-10-281-867-3	Sequence 3, Appli
	28	39.8	4.7	2527	3	US-09-949-016-2205	Sequence 2205, Ap
	29	39.6	4.7	3289	3	US-09-587-945-1	Sequence 1, Appli
	30	39.4	4.7	7847	3	US-09-799-451-591	Sequence 591, App
c	31	38.4	4.5	7218	2	US-08-232-463-14	Sequence 14, Appl
c	32	38	4.5	116955	3	US-09-949-016-17565	Sequence 17565, A
	33	37.6	4.4	601	3	US-09-949-016-206248	Sequence 206248,
c	34	37.2	4.4	1440	2	US-08-224-482-5	Sequence 5, Appli
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c	36	37.2	4.4	2811	2	US-08-040-548-31	Sequence 31, Appl
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c	43	37	4.4	2325	3	US-09-252-991A-12916	Sequence 12916, A
	44	36.8	4.3	432	3	US-09-060-299-5	Sequence 5, Appli
	45	36.8	4.3	432	3	US-09-402-923A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-023-655-1175
; Sequence 1175, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g188623

US-09-023-655-1175

Query Match 79.7%; Score 674; DB 3; Length 1349;
Best Local Similarity 83.9%; Pred. No. 3.8e-179;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

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Qy        679 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 738
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RESULT 2
US-08-085-122-12
; Sequence 12, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..1054
US-08-085-122-12

Query Match 79.7%; Score 674; DB 2; Length 1400;
Best Local Similarity 83.9%; Pred. No. 3.9e-179;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:30:50 ; Search time 778.807 Seconds
(without alignments)
8982.829 Million cell updates/sec

Title: US-10-679-951-1
Perfect score: 846
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	846	100.0	846	8	US-10-679-951-1	Sequence 1, Appli
2	674	79.7	1008	8	US-10-679-951-7	Sequence 7, Appli
3	674	79.7	1318	7	US-10-384-339C-31	Sequence 31, Appl
4	674	79.7	1349	7	US-10-641-643-1175	Sequence 1175, Ap
5	674	79.7	1363	5	US-10-193-656-5	Sequence 5, Appli
6	674	79.7	1740	8	US-10-783-528-39	Sequence 39, Appl
7	674	79.7	1743	6	US-10-177-293-361	Sequence 361, App
8	674	79.7	1743	6	US-10-172-118-799	Sequence 799, App
9	674	79.7	1743	6	US-10-388-360-372	Sequence 372, App
10	674	79.7	1743	6	US-10-295-027-1110	Sequence 1110, Ap
11	674	79.7	1743	7	US-10-429-160-74	Sequence 74, Appl
12	674	79.7	1743	7	US-10-342-887-799	Sequence 799, App
13	674	79.7	1743	8	US-10-723-860-2343	Sequence 2343, Ap
14	674	79.7	1883	8	US-10-357-930-24813	Sequence 24813, A
15	674	79.7	1887	8	US-10-723-860-6539	Sequence 6539, Ap
16	669.8	79.2	873	8	US-10-679-951-5	Sequence 5, Appli
17	641.8	75.9	1601	5	US-10-087-192-1805	Sequence 1805, Ap
18	633.6	74.9	1609	6	US-10-240-965-116	Sequence 116, App
19	567.8	67.1	952	7	US-10-755-889-423	Sequence 423, App
20	566	66.9	711	8	US-10-679-951-3	Sequence 3, Appli
21	493	58.3	539	7	US-10-283-975A-24	Sequence 24, Appl
22	423	50.0	1097	7	US-10-240-425-1547	Sequence 1547, Ap
23	423	50.0	1097	7	US-10-717-597-101	Sequence 101, App
24	313.8	37.1	483	3	US-09-919-580-200	Sequence 200, App
25	312.4	36.9	419	3	US-09-918-995-35682	Sequence 35682, A
26	281.6	33.3	409	3	US-09-813-358-205	Sequence 205, App
27	281.6	33.3	409	3	US-09-997-279-205	Sequence 205, App
28	255	30.1	739	3	US-09-962-832-120	Sequence 120, App
29	255	30.1	739	8	US-10-482-029-159	Sequence 159, App
30	255	30.1	739	9	US-10-843-641A-6006	Sequence 6006, Ap
31	255	30.1	41966	5	US-10-087-192-1804	Sequence 1804, Ap
32	229.8	27.2	1272	7	US-10-152-319A-1705	Sequence 1705, Ap
33	222.6	26.3	984	5	US-10-087-192-1802	Sequence 1802, Ap
c 34	147.4	17.4	521	6	US-10-029-386-7358	Sequence 7358, Ap
c 35	147	17.4	148	6	US-10-029-386-21058	Sequence 21058, A
c 36	117	13.8	561	6	US-10-029-386-11796	Sequence 11796, A
c 37	111	13.1	112	6	US-10-029-386-25496	Sequence 25496, A
38	104	12.3	406	5	US-10-066-543-1724	Sequence 1724, Ap
39	104	12.3	406	5	US-10-066-543-2399	Sequence 2399, Ap
40	99.8	11.8	431	8	US-10-357-930-37459	Sequence 37459, A
41	88.2	10.4	275	8	US-10-357-930-7499	Sequence 7499, Ap
42	86	10.2	32963	5	US-10-087-192-1801	Sequence 1801, Ap
43	76	9.0	76	8	US-10-714-195-72	Sequence 72, Appl
44	76	9.0	76	9	US-10-852-797-352	Sequence 352, App
45	50.2	5.9	289	3	US-09-783-590-12057	Sequence 12057, A

ALIGNMENTS

RESULT 1
US-10-679-951-1
; Sequence 1, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-679-951-1

Query Match 100.0%; Score 846; DB 8; Length 846;
Best Local Similarity 100.0%; Pred. No. 1.8e-257;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 7, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-679-951-7

Query Match 79.7%; Score 674; DB 8; Length 1008;
Best Local Similarity 83.9%; Pred. No. 7.2e-203;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        679 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 738
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GenCore version 5.1.6
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1875.453 Million cell updates/sec

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Perfect score: 846
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	674	79.7	1743	6	US-10-826-585-57	Sequence 57, Appl
	2	250.8	29.6	600	8	US-11-128-061-4364	Sequence 4364, Ap
	3	250.8	29.6	600	8	US-11-128-049-4364	Sequence 4364, Ap
	4	250.8	29.6	972	8	US-11-128-061-722	Sequence 722, App
	5	250.8	29.6	972	8	US-11-128-049-722	Sequence 722, App
	6	229	27.1	1277	8	US-11-136-527-2432	Sequence 2432, Ap
	7	122.4	14.5	600	8	US-11-136-527-6528	Sequence 6528, Ap
	8	95	11.2	1040	7	US-10-750-185-56698	Sequence 56698, A
	9	95	11.2	1040	7	US-10-750-623-56698	Sequence 56698, A
	10	39.6	4.7	1506	7	US-10-971-560-9	Sequence 9, Appli
	11	39.6	4.7	3289	7	US-10-971-560-8	Sequence 8, Appli
	12	39.6	4.7	4158	7	US-10-971-560-3	Sequence 3, Appli
	13	39.6	4.7	6458	7	US-10-971-560-1	Sequence 1, Appli
	14	36.8	4.3	300	8	US-11-136-527-482	Sequence 482, App
	15	36.8	4.3	300	8	US-11-136-527-4578	Sequence 4578, Ap
	16	36.8	4.3	5100	8	US-11-108-528-79	Sequence 79, Appl
	17	34	4.0	649	7	US-10-516-768-7	Sequence 7, Appli
	18	33.6	4.0	3703	7	US-10-750-185-27363	Sequence 27363, A
	19	33.6	4.0	3703	7	US-10-750-623-27363	Sequence 27363, A
	20	33.6	4.0	5119	8	US-11-108-528-81	Sequence 81, Appl
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	22	33.4	3.9	1625	7	US-10-750-623-43394	Sequence 43394, A
	23	33.2	3.9	1400	8	US-11-136-527-6127	Sequence 6127, Ap
	24	33.2	3.9	1447	8	US-11-136-527-2031	Sequence 2031, Ap
c	25	33	3.9	1662	8	US-11-136-619-3	Sequence 3, Appli
c	26	32.8	3.9	879	8	US-11-143-401-46	Sequence 46, Appl
	27	32.8	3.9	2323	8	US-11-186-284-62	Sequence 62, Appl
	28	32.8	3.9	2641	7	US-10-947-249-179	Sequence 179, App
c	29	32.8	3.9	12732	7	US-10-802-796-1	Sequence 1, Appli
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	37	32.6	3.9	157224	8	US-11-112-908-51	Sequence 51, Appl
	38	32.6	3.9	161726	8	US-11-112-908-48	Sequence 48, Appl
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	43	32.4	3.8	8354	8	US-11-113-424-13	Sequence 13, Appl
c	44	32.2	3.8	507	7	US-10-467-657-547	Sequence 547, App
	45	32.2	3.8	1044	7	US-10-508-263-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-10-826-585-57
; Sequence 57, Application US/10826585
; Publication No. US20060008807A1
; GENERAL INFORMATION:
; APPLICANT: Immunivest Corporation
; APPLICANT: O'Hara, Shawn Mark
; APPLICANT: Foulk, Brad
; APPLICANT: Zweitzig, Daniel
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
; TITLE OF INVENTION: morphological features on the same sample
; FILE REFERENCE: IMMC 143 PCT/US
; CURRENT APPLICATION NUMBER: US/10/826,585
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/369945
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/330669
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/26867
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Human
US-10-826-585-57

Query Match 79.7%; Score 674; DB 6; Length 1743;
Best Local Similarity 83.9%; Pred. No. 3.1e-173;
Matches 846; Conservative 0; Mismatches 0; Indels 162; Gaps 1;

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Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 486

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 546

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 606

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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```
Db        607 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 666

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300

Db        667 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 726

Qy        301 GGCAACTCT--------------------------------------------------- 309

Db        727 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 786

Qy        310 ------------------------------------------------------------ 309

Db        787 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 846

Qy        310 ----------------------------------------------------GGGCGTCCA 318

Db        847 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGGGCGTCCA 906

Qy        319 AAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGCTGCCCGGGCTCCAATGGT 378

Db        907 AAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGCTGCCCGGGCTCCAATGGT 966

Qy        379 TTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAACACCACCAAATGCAACGAG 438

Db        967 TTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAACACCACCAAATGCAACGAG 1026

Qy        439 GGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 498

Db       1027 GGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 1086

Qy        499 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 558

Db       1087 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 1146

Qy        559 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 618

Db       1147 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 1206

Qy        619 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 678

Db       1207 AGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATG 1266

Qy        679 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 738

Db       1267 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 1326

Qy        739 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 798

Db       1327 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 1386

Qy        799 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 846

Db       1387 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1434
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RESULT 2
US-11-128-061-4364
; Sequence 4364, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061

; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4364
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-4364

Query Match 29.6%; Score 250.8; DB 8; Length 600;
Best Local Similarity 66.2%; Pred. No. 1.6e-58;
Matches 388; Conservative 0; Mismatches 177; Indels 21; Gaps 1;

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Qy        258 CAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAGGGCAACTCTGGGCGTCC 317
Db         36 CCGCTATCCCGGAGAACAGTGTGTTGAGGTGGTCACCCTACGGAGCACGGAAAGGAGTCT 95

Qy        318 AAAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGCTGCCCGGGCTCCAATGG 377
Db         96 GAAGGATGAGAACTACACCAGAGGCTGTGGCAGTCTTCCCGGGTGCCCGGGCATAGCCGG 155

Qy        378 TTTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAACACCACCAAATGCAACGA 437
Db        156 TTTCCATGGCAACCACACCTTCCACTTCCTGAGATGCTGCAACTCCACCCACTGCAATGG 215

Qy        438 GGGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAA 497
Db        216 CGGCCCAGTTCTAAATCTTCGGGACTTACCACCGAATGGCGTCCAGTGTTACAGCTGCGA 275

Qy        498 GGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCC 557
Db        276 GGGCAACAGCACCCACGGGTGTTCCTCCAAAGAGACTTCCCTCGTTGACTGCCGGGGACC 335

Qy        558 CATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGT 617
Db        336 GATGGATCAGTGCCTGGAGGCCACCGGCTTGGATGTGCTGGCAAACCGGAGTCACACCGT 395

Qy        618 AAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCAT 677
Db        396 GAGAGGCTGCTCGACGGCTTCCTGGTGCCCAGGCTCCCATGTGGCAGATGCCTTCCTCCT 455

Qy        678 GAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGT 737
Db        456 GAGCCACCCCAACATCTCGTGCTGTGATGGCAGCGGCTGTAATGGACC------------ 503

Qy        738 CCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCAC 797
Db        504 ---------CAGAAGCGGCGCCCCCAGGACAGACCCTGCTCGTCTAGGCCTCATCGTCTC 554

Qy        798 CCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACC 843
Db        555 CCTGCTCCTGACCGTCAGACTGTGGGGAGGCACTCTCCTCTGGACC 600
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RESULT 3
US-11-128-049-4364
; Sequence 4364, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:03 ; Search time 74.1673 Seconds
(without alignments)
1664.689 Million cell updates/sec

Title: US-10-679-951-2
Perfect score: 1583
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1583	100.0	281	6	ABP60419	Abp60419 Human uPA
2	1546	97.7	335	1	AAP60436	Aap60436 Sequence
3	1546	97.7	335	2	AAR07561	Aar07561 Recombina
4	1546	97.7	335	2	AAR44424	Aar44424 Human pho
5	1546	97.7	335	2	AAR58707	Aar58707 Human pho
6	1546	97.7	335	2	AAR97612	Aar97612 Human uro
7	1546	97.7	335	2	AAW31165	Aaw31165 Human pho
8	1546	97.7	335	4	AAU04454	Aau04454 Human uro
9	1546	97.7	335	6	AAE37129	Aae37129 Human uro
10	1546	97.7	335	6	ABR47562	Abr47562 Breast ca
11	1546	97.7	335	6	ABP60422	Abp60422 Human uPA
12	1546	97.7	335	7	ADN40009	Adn40009 Cancer/an
13	1546	97.7	335	8	ADJ45544	Adj45544 LXR-ligan
14	1546	97.7	335	8	ADO47984	Ado47984 Human uro
15	1546	97.7	335	8	ADP12460	Adp12460 Protein e
16	1546	97.7	335	8	ADQ19525	Adq19525 Human sof
17	1546	97.7	335	8	ADP24414	Adp24414 PRO polyp
18	1546	97.7	335	8	ADR46684	Adr46684 Cancer-as
19	1541	97.3	335	2	ABU10413	Abu10413 Human uro
20	1539	97.2	335	2	AAY04103	Aay04103 Urokinase
21	1535	97.0	335	4	AAU07610	Aau07610 Human u-P
22	1533	96.8	335	3	AAB26241	Aab26241 Human uro
23	1517	95.8	330	9	AEB54709	Aeb54709 Human pla
24	1473	93.1	359	6	ABU11701	Abu11701 Human MDD
25	1354	85.5	299	4	AAU07611	Aau07611 Human u-P
26	1353	85.5	301	8	ADR14423	Adr14423 Human NF-
27	1293.5	81.7	290	6	ABP60421	Abp60421 Human uPA
28	1271.5	80.3	236	6	ABP60420	Abp60420 Human uPA
29	1263	79.8	287	7	ABM85797	Abm85797 Human pro
30	1259	79.5	283	9	AEA35322	Aea35322 Human mat
31	1249	78.9	283	8	ADU73621	Adu73621 Urokinase
32	1232.5	77.9	286	8	ABM84629	Abm84629 Human dia
33	1084	68.5	281	6	ABU89746	Abu89746 Protein d
34	997	63.0	174	1	AAP60435	Aap60435 Sequence
35	997	63.0	174	2	AAR44423	Aar44423 Peptide c
36	997	63.0	174	2	AAR58710	Aar58710 Human PIP
37	997	63.0	174	2	AAW31168	Aaw31168 hPIP part
38	911	57.5	327	7	ABM85796	Abm85796 Mouse pro
39	515	32.5	90	2	ABU10417	Abu10417 Human uro
40	515	32.5	90	2	AAY04101	Aay04101 Urokinase
41	515	32.5	90	4	AAU04458	Aau04458 Human u-P
42	448	28.3	92	2	AAW99896	Aaw99896 Urokinase
43	448	28.3	92	4	AAU04456	Aau04456 Human u-P
44	440	27.8	92	2	ABU10415	Abu10415 Human uro
45	363	22.9	94	1	AAP60434	Aap60434 Sequence

ALIGNMENTS

RESULT 1
ABP60419
ID ABP60419 standard; protein; 281 AA.
XX
AC ABP60419;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human uPAR exon 4 deletion variant protein SEQ ID NO 2.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; receptor.
XX
OS Homo sapiens.
XX
PN DE10117381-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001DE-01017381.
XX
PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR N-PSDB; ABZ26096.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 1; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a
CC urokinase type plasminogen activator receptor (uPAR) which has one or two
CC exons of the native sequence at least partly missing, excluding Genbank
CC sequence U08839. Molecules of the invention are used to diagnose,
CC prognose and treat cancer, particularly breast or ovarian cancer. The
CC present sequence is that of a uPAR exon 4 deletion variant protein of the
CC invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1583; DB 6; Length 281;

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  Best Local Similarity   100.0%;  Pred. No. 1.9e-115;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPG 120

Qy        121 CPGSNGFHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CPGSNGFHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFL 180

Qy        181 IDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCN 240

Qy        241 HPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
              |||||||||||||||||||||||||||||||||||||||||
Db        241 HPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
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RESULT 2
AAP60436
ID AAP60436 standard; protein; 335 AA.
XX
AC AAP60436;
XX
DT 25-JUN-1991 (first entry)
XX
DE Sequence of human phospholipase inhibitory protein (hPIP) encoded by pLE-
DE 1.
XX
KW Anti-inflammatory; phospholipase inhibitor; inflammatory disorder;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO8606100-A.
XX
PD 23-OCT-1986.
XX
PF 14-APR-1986; 86WO-US000772.
XX
PR 15-APR-1985; 85US-00723046.
XX
PA (BIOT-) BIOTECHN RES PARTN.
XX
PI Johnson LF, Longenecke J;
XX
DR WPI; 1986-291667/44.
DR N-PSDB; AAN60374.
XX
PT Human antiinflammatory phospholipase inhibitor protein - obtd. by
PT purificn. of human inter:peritoneal dialysis fluid.
XX
PS Claim 2; Fig 13; 61pp; English.
XX
CC Lambda U200 was used to probe cDNA libraries for hPIP. Lambda U200 and
CC lambda U500 share approximately 50 bp at the 5' ends of each and then
CC diverge. This divergence was due to intron splicing. PMN600 not only
CC shares the 50 bp segment common to lambda U200 and lambda U500, but its
CC homology with lambda U500 extends for another approximately 200 bp. These
CC sequences then also diverge. This divergence was shown to be due to the
CC presence of optional 3' terminal exons in the gene. pLE-1 contains the
CC full-length coding sequence for hPIP. The hPIP can be used for producing
CC antibodies (claimed). The PIP proteins show in vitro activity as
CC phospholipase inihibitors. The proteins are useful both to control
CC inflammatory responses and to treat inflammatory disorders
XX
SQ Sequence 335 AA;

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  Query Match             97.7%;  Score 1546;  DB 1;  Length 335;
  Best Local Similarity   83.9%;  Pred. No. 1.8e-112;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
              ||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 -----------------------------------GRPKDDRHLRGCGYLPGCPGSNG 126
                                                  |||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        127 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        187 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        247 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
              |||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335
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RESULT 3
AAR07561
ID AAR07561 standard; protein; 335 AA.
XX
AC AAR07561;
XX
DT 25-MAR-2003 (revised)
DT 06-FEB-1991 (first entry)
XX
DE Recombinant urokinase-type plasminogen activator receptor.
XX
KW Recombinant urokinase-type plasminogen activator receptor; antibody;
KW u-PAR; cancer therapy; metastasis; p-uPAR-1.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .22
FT   /label= signal_peptide
FT Peptide   23. .335
FT   /label= mature_peptide
FT Region   23. .47
FT   /note= "sequence determined on purified protein"
FT Domain   304. .320
FT   /label= transmembrane_domain
XX
PN WO9012091-A.
XX
PD 18-OCT-1990.
XX
PF 07-APR-1989; 89US-00334613.
XX
PR 07-APR-1989; 89US-00334613.
PR 03-JUL-1989; 89US-00374854.
XX
PA (CANC-) CANCER FORSKNINGSFONDET AF 1989.
XX
PI Dano K, Blasi F, Roldan A, Cubellis M, Masucci M, Appella E;
PI Schleuning W, Behrendt;
XX
DR WPI; 1990-334842/44.
DR N-PSDB; AAQ06354.
XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:58 ; Search time 12.5353 Seconds
(without alignments)
2156.859 Million cell updates/sec

Title: US-10-679-951-2
Perfect score: 1583
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1546	97.7	335	2	A39743	u-plasminogen acti
2	1084	68.5	281	2	S39495	u-plasminogen acti
3	991.5	62.6	330	1	JN0561	urokinase-type pla
4	911	57.5	327	2	A55356	urokinase-type pla
5	897.5	56.7	328	2	S42152	urinary plasminoge
6	367	23.2	222	2	B41643	urokinase-type pla
7	365	23.1	222	2	B55356	urokinase-type pla
8	129.5	8.2	1046	2	A26838	prestalk protein p
9	119	7.5	601	2	D89711	protein F40E10.4 [
10	119	7.5	601	2	T22025	hypothetical prote
11	119	7.5	2090	2	T30075	hypothetical prote
12	119	7.5	2153	2	T30074	hypothetical prote
13	118.5	7.5	1135	1	JQ1928	G2-G1 polyprotein
14	118.5	7.5	1574	2	T13954	MEGF6 protein - ra
15	118.5	7.5	2871	2	A55624	fibrillin-1 precur
16	117	7.4	589	2	T43210	fibulin-1D precurs
17	117	7.4	2531	2	S18188	notch protein homo
18	117	7.4	2531	2	A46019	notch-1 protein -
19	116.5	7.4	689	2	T42760	fibulin, splice fo
20	116.5	7.4	712	2	T42990	fibulin 1, splice
21	115.5	7.3	686	2	JC7569	Delta-4 protein -
22	112.5	7.1	685	2	JC7570	Delta-4 protein -
23	112	7.1	798	2	T22793	hypothetical prote
24	112	7.1	2139	2	A35672	crumbs protein - f
25	111	7.0	2871	2	A55567	fibrillin I - bovi
26	110	6.9	3002	2	A47221	fibrillin 1 precur
27	109.5	6.9	2907	2	A57278	fibrillin-2 precur
28	109	6.9	313	2	S44208	extracellular matr
29	109	6.9	1786	1	MMHUB1	laminin beta-1 cha
30	108.5	6.9	1110	1	B42544	G2-G1 polyprotein
31	108.5	6.9	1620	2	T27283	hypothetical prote
32	108.5	6.9	1895	2	T15881	hypothetical prote
33	107.5	6.8	86	1	V6EP9A	venom protein C9S3
34	107.5	6.8	909	1	QRXLL1	LDL receptor 1 pre
35	107	6.8	769	1	IJHULM	leukocyte adhesion
36	107	6.8	2524	2	A35844	Xotch protein - Af
37	106.5	6.7	185	1	JC2394	phospholipase A2 i
38	106.5	6.7	2918	2	A54105	fibrillin-2 precur
39	106	6.7	835	2	JP0076	nel protein - chic
40	104.5	6.6	2555	2	A40043	notch protein homo
41	103.5	6.5	251	2	A55035	cysteine-rich prot
42	103	6.5	200	1	A54020	Crotalus neutraliz
43	103	6.5	719	2	T00266	hypothetical prote
44	103	6.5	1101	2	T16840	hypothetical prote
45	102	6.4	862	1	QRMSLD	LDL receptor precu

ALIGNMENTS

RESULT 1
A39743
u-plasminogen activator receptor form 1 precursor - human
N;Alternate names: monocyte activation antigen Mo3; urokinase-type plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: S12376; A39743; A35242; S34461; I56138; S67529; I39206
R;Roldan, A.L.; Cubellis, M.V.; Masucci, M.T.; Behrendt, N.; Lund, L.R.; Dano, K.; Appel
EMBO J. 9, 467-474, 1990
A;Title: Cloning and expression of the receptor for human urokinase plasminogen activato
A;Reference number: S12376; MUID:90151622; PMID:1689240
A;Accession: S12376
A;Molecule type: mRNA
A;Residues: 1-335 <ROL>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:X51675; NID:g37604; PIDN:CAA35981.1; PID:g
R;Behrendt, N.; Ploug, M.; Patthy, L.; Houen, G.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 7842-7847, 1991
A;Title: The ligand-binding domain of the cell surface receptor for urokinase-type plasm
A;Reference number: A39743; MUID:91210310; PMID:1850423
A;Accession: A39743
A;Molecule type: protein
A;Residues: 23-24,'X',26-27,'XX',30-33,'X',35-38,'X',40,'X',42;110-116,'XX',119,'X' <BEH
A;Cross-references: UNIPARC:UPI00001770BD; UNIPARC:UPI00001770BE
R;Behrendt, N.; Ronne, E.; Ploug, M.; Petri, T.; Lober, D.; Nielsen, L.S.; Schleuning, W
J. Biol. Chem. 265, 6453-6460, 1990
A;Title: The human receptor for urokinase plasminogen activator. NH-2-terminal amino aci
A;Reference number: A35242; MUID:90202929; PMID:2156852
A;Accession: A35242
A;Molecule type: protein
A;Residues: 23,'X',25-38,'H',40-43,'X',45,'X',47-51,'X' <BE2>
A;Cross-references: UNIPARC:UPI0000143F2B
A;Note: the authors show a tentative identification of His for residue 39
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase p
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34461
A;Molecule type: mRNA
A;Residues: 246-335 <PYK>
A;Cross-references: UNIPARC:UPI00001770BF
R;Ploug, M.; Ronne, E.; Behrendt, N.; Jensen, A.L.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 1926-1933, 1991
A;Title: Cellular receptor for urokinase plasminogen activator. Carboxyl-terminal proces
A;Reference number: A38677; MUID:91107700; PMID:1846368
A;Contents: annotation
R;Min, H.Y.; Semnani, R.; Mizukami, I.F.; Watt, K.; Todd, R.F.
J. Immunol. 148, 3636-3642, 1992
A;Title: cDNA for Mo3, a monocyte activation antigen, encodes the human receptor for uro
A;Reference number: I56138; MUID:92268511; PMID:1316922
A;Accession: I56138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A;Residues: 1-335 <RES>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:M83246; NID:g188623; PIDN:AAA59862.1; PID:
R;Wang, Y.; Dang, J.; Johnson, L.K.; Selhamer, J.J.; Doe, W.F.
Eur. J. Biochem. 227, 116-122, 1995
A;Title: Structure of the human urokinase receptor gene and its similarity to CD59 and t
A;Reference number: S67529; MUID:95154279; PMID:7531640
A;Accession: S67529
A;Molecule type: DNA
A;Residues: 1-335 <WAN>
A;Cross-references: UNIPARC:UPI000000D8C1
A;Note: the authors translated the codon CGC for residue 51 as Ala
R;Casey, J.R.; Petranka, J.G.; Kottra, J.; Fleenor, D.E.; Rosse, W.F.
Blood 84, 1151-1156, 1994
A;Title: The structure of the urokinase-type plasminogen activator receptor gene.
A;Reference number: I39206; MUID:94325556; PMID:8049431
A;Accession: I39206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <RE2>
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C;Genetics:
A;Gene: uPAR
A;Introns: 19/1; 56/1; 104/1; 158/1; 203/1; 252/1
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; glycoprotein; membrane protein; phosphatidylinositol l
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F;23-304/Product: (or 23-305 or 23-306) u-plasminogen activator receptor #status experim
F;23-107/Domain: Ly-6 homology <LY6A>
F;115-206/Domain: Ly-6 homology <LY6B>
F;214-301/Domain: Ly-6 homology <LY6C>
F;74,184,194,222,255/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Matches 281; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

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Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
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Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 -----------------------------------GRPKDDRHLRGCGYLPGCPGSNG 126
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Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        127 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        187 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 246
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Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        247 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
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RESULT 2
S39495
u-plasminogen activator receptor form 2 precursor - human
N;Alternate names: urokinase-type plasminogen activator receptor form 2
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S39495; S34462
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
submitted to the EMBL Data Library, December 1993
A;Description: An alternatively spliced variant of mRNA for the human receptor for uroki
A;Reference number: S39495
A;Accession: S39495
A;Molecule type: mRNA
A;Residues: 1-281 <PYK1>
A;Cross-references: UNIPROT:Q03405; UNIPARC:UPI000002B696; EMBL:X74039; NID:g456192; PIDN
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; Da
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase pl
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34462
A;Molecule type: mRNA
A;Residues: 246-281 <PYK2>
A;Cross-references: UNIPARC:UPI000016A0A4; GB:U09347; GB:S63673; NID:g483827; PIDN:AAA17
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; receptor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-281/Product: u-plasminogen activator receptor #status predicted <MAT>
F;115-206/Domain: Ly-6 homology <LY6>

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Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 -----------------------------------GRPKDDRHLRGCGYLPGCPGSNG 126
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Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        127 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 186
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Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        187 MNQCLVATGTHE 198
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Db        241 MNQCLVATGTHE 252
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RESULT 3
JN0561
urokinase-type plasminogen activator receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: JN0561; I46977
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and induc
A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0561
A;Molecule type: mRNA
A;Residues: 1-330 <KRA>
A;Cross-references: UNIPROT:Q05588; UNIPARC:UPI0000137CC6; GB:L03545; NID:g163802; PIDN:
R;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U.
Thromb. Res. 72, 59-70, 1993
A;Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen activator r
A;Reference number: I46977; MUID:94167671; PMID:8122188
A;Accession: I46977
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <REU>
A;Cross-references: UNIPARC:UPI0000137CC6; GB:S70635; NID:g545770; PIDN:AAB30120.1; PID:
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-300/Product: urokinase-type plasminogen activator receptor #status predicted <MAT>
F;21-104/Domain: Ly-6 homology <LY6A>
F;113-201/Domain: Ly-6 homology <LY6B>
F;209-296/Domain: Ly-6 homology <LY6C>
F;301-330/Domain: carboxyl-terminal propeptide #status predicted <CPRO>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:28 ; Search time 67.5514 Seconds
(without alignments)
2934.852 Million cell updates/sec

Title: US-10-679-951-2
Perfect score: 1583
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1546	97.7	335	1	UPAR_HUMAN	Q03405 homo sapien
2	1544	97.5	335	1	UPAR_PANTR	Q9gk80 pan troglod
3	1486	93.9	335	1	UPAR_CERAE	Q9gk79 cercopithec
4	1475	93.2	335	1	UPAR_MACFA	Q9gk78 macaca fasc
5	1353	85.5	301	2	Q9BWT0_HUMAN	Q9bwt0 homo sapien
6	1231.5	77.8	336	2	Q9GK77_AOTTR	Q9gk77 aotus trivi
7	1084	68.5	281	2	Q6IB52_HUMAN	Q6ib52 homo sapien
8	1079	68.2	251	2	Q9UPI5_HUMAN	Q9upi5 homo sapien
9	991.5	62.6	330	1	UPAR_BOVIN	Q05588 bos taurus
10	926.5	58.5	328	2	O35771_RAT	O35771 rattus norv
11	911	57.5	327	1	UPAR_MOUSE	P35456 mus musculu
12	911	57.5	327	2	Q545X5_MOUSE	Q545x5 mus musculu
13	904.5	57.1	322	2	Q9R119_CRIGR	Q9r119 cricetulus
14	863.5	54.5	328	1	UPAR_RAT	P49616 rattus norv
15	560.5	35.4	204	2	Q9TVA9_BOVIN	Q9tva9 bos taurus
16	367	23.2	222	1	UPAS_MOUSE	P35457 mus musculu
17	365	23.1	222	2	Q91Z14_MOUSE	Q91z14 mus musculu
18	352.5	22.3	220	1	UPAS_RAT	P51573 rattus norv
19	256.5	16.2	88	2	Q9N124_HORSE	Q9n124 equus cabal
20	162.5	10.3	205	2	Q4FAG4_9SALA	Q4fag4 plethodon m
21	160	10.1	39	2	Q4RCT4_TETNG	Q4rct4 tetraodon n
22	159.5	10.1	205	2	Q4FAH3_9SALA	Q4fah3 plethodon m
23	158.5	10.0	199	2	Q4FAE1_9SALA	Q4fae1 plethodon s
24	158.5	10.0	205	2	Q4FAH1_9SALA	Q4fah1 plethodon m
25	157.5	9.9	205	2	Q4FAG7_PLEJO	Q4fag7 plethodon j
26	157.5	9.9	205	2	Q4FAG5_9SALA	Q4fag5 plethodon s
27	157.5	9.9	205	2	Q4FAG6_9SALA	Q4fag6 plethodon c
28	157	9.9	217	2	Q566G7_XENLA	Q566g7 xenopus lae
29	156.5	9.9	196	2	Q4FAD0_9SALA	Q4fad0 aneides fer
30	156.5	9.9	199	2	Q4FAG8_9SALA	Q4fag8 plethodon m
31	156.5	9.9	205	2	Q4FAH4_9SALA	Q4fah4 plethodon t
32	151.5	9.6	196	2	Q4FAD1_9SALA	Q4fad1 aneides fer
33	151.5	9.6	199	2	Q4FAG2_9SALA	Q4fag2 plethodon t
34	150.5	9.5	199	2	Q4FAG9_9SALA	Q4fag9 plethodon w
35	150.5	9.5	199	2	Q4FAD9_9SALA	Q4fad9 desmognathu
36	149.5	9.4	205	2	Q4FAG0_PLEJO	Q4fag0 plethodon j
37	149.5	9.4	205	2	Q4FAF6_9SALA	Q4faf6 plethodon c
38	148	9.3	200	2	Q78CF9_NOTAT	Q78cf9 notechis at
39	148	9.3	200	2	Q9PRF7_9SAUR	Q9prf7 notechis sc
40	148	9.3	201	2	Q9PTC7_OXYMI	Q9ptc7 oxyuranus m
41	147.5	9.3	199	2	Q4FAH2_9SALA	Q4fah2 plethodon w
42	147.5	9.3	254	2	O95053_HUMAN	O95053 homo sapien
43	147	9.3	200	2	Q9PTC9_9SAUR	Q9ptc9 oxyuranus s
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45	145.5	9.2	199	2	Q4FAF7_9SALA	Q4faf7 plethodon t

ALIGNMENTS

RESULT 1
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AC Q03405; Q12876; Q15845; Q16887; Q9NYC8; Q9UD69; Q9UEA6; Q9UM92;
AC Q9UMV0;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE PAR) (Monocyte activation antigen Mo3) (CD87 antigen).
GN Name=PLAUR; Synonyms=MO3, UPAR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-33.
RX MEDLINE=90151622; PubMed=1689240;
RA Roldan A.L., Cubellis M.V., Masucci M.T., Behrendt N., Lund L.R.,
RA Danoe K., Appella E., Blasi F.;
RT "Cloning and expression of the receptor for human urokinase
RT plasminogen activator, a central molecule in cell surface, plasmin
RT dependent proteolysis.";
RL EMBO J. 9:467-474(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=92268511; PubMed=1316922;
RA Min H.Y., Semnani R., Mizukami I.F., Watt K., Todd R.F. III, Liu D.Y.;
RT "cDNA for Mo3, a monocyte activation antigen, encodes the human
RT receptor for urokinase plasminogen activator.";
RL J. Immunol. 148:3636-3642(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RX MEDLINE=94178507; PubMed=8131971;
RA Bayraktutan U., Jones P.;
RT "A novel urokinase receptor on monocyte-like macrophage cell line.";
RL Biochem. Soc. Trans. 21:395-395(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX MEDLINE=93314820; PubMed=8392005; DOI=10.1016/0014-5793(93)81763-P;
RA Pyke C., Eriksen J., Solberg H., Schnack Nielsen B., Kristensen P.,
RA Lund L.R., Danoe K.;
RT "An alternatively spliced variant of mRNA for the human receptor for
RT urokinase plasminogen activator.";
RL FEBS Lett. 326:69-74(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 3).
RC TISSUE=Placenta;
RX MEDLINE=94325556; PubMed=8049431;
RA Casey J.R., Petranka J.G., Kottra J., Fleenor D.E., Rosse W.F.;
RT "The structure of the urokinase-type plasminogen activator receptor
RT gene.";
RL Blood 84:1151-1156(1994).

RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLY-55; ALA-86;
RP GLN-105; ARG-220; LYS-281 AND PRO-317.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP NUCLEOTIDE SEQUENCE OF 1-322 (ISOFORM 1).
RC TISSUE=Lung cancer;
RA Zhu F., Jia S., He F.;
RT "Molecular cloning of UPAR from a human giant cell lung cancer cell
RT line.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE OF 1-18.
RX MEDLINE=95329719; PubMed=7605992;
RA Soravia E., Grebe A., De Luca P., Helin K., Suh T.T., Degen J.L.,
RA Blasi F.;
RT "A conserved TATA-less proximal promoter drives basal transcription
RT from the urokinase-type plasminogen activator receptor gene.";
RL Blood 86:624-635(1995).
RN [11]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=90202929; PubMed=2156852;
RA Behrendt N., Roenne E., Ploug M., Petri T., Loeber D., Nielsen L.S.,
RA Schleuning W.-D., Blasi F., Appella E., Danoe K.;
RT "The human receptor for urokinase plasminogen activator. NH2-terminal
RT amino acid sequence and glycosylation variants.";
RL J. Biol. Chem. 265:6453-6460(1990).
RN [12]
RP PROTEIN SEQUENCE OF 106-116, AND CLEAVAGE BY U-PA.
RX MEDLINE=97182578; PubMed=9030717;
RA Hoeyer-Hansen G., Ploug M., Behrendt N., Roenne E., Danoe K.;
RT "Cell-surface acceleration of urokinase-catalyzed receptor cleavage.";
RL Eur. J. Biochem. 243:21-26(1997).
RN [13]
RP DISULFIDE BONDS, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=93352546; PubMed=8394346;
RA Ploug M., Kjalke M., Roenne E., Weidle U., Hoeyer-Hansen G., Danoe K.;
RT "Localization of the disulfide bonds in the NH2-terminal domain of the
RT cellular receptor for human urokinase-type plasminogen activator. A
RT domain structure belonging to a novel superfamily of glycolipid-
RT anchored membrane proteins.";
RL J. Biol. Chem. 268:17539-17546(1993).
CC -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC Plays a role in localizing and promoting plasmin formation.
CC Mediates the proteolysis-independent signal transduction
CC activation effects of U-PA. It is subject to negative-feedback
CC regulation by U-PA which cleaves it into an inactive form.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (isoform 1). Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=uPAR1, GPI-anchored;
CC IsoId=Q03405-1; Sequence=Displayed;
CC Name=2; Synonyms=uPAR2, Secreted;
CC IsoId=Q03405-2; Sequence=VSP_006715;
CC Name=3;
CC IsoId=Q03405-3; Sequence=VSP_006714;
CC -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC --
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC --
DR EMBL; X51675; CAA35981.1; -; mRNA.
DR EMBL; M83246; AAA59862.1; -; mRNA.
DR EMBL; X74039; CAA52191.1; -; mRNA.
DR EMBL; U09346; AAA17979.1; -; Unassigned_DNA.
DR EMBL; U09347; AAA17978.1; -; mRNA.
DR EMBL; U09937; AAB60690.1; -; Genomic_DNA.
DR EMBL; U09931; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09932; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09933; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09935; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09936; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U08839; AAB60333.1; -; mRNA.
DR EMBL; AY194849; AAN86351.1; -; Genomic_DNA.
DR EMBL; AC005525; AAC32739.1; -; Genomic_DNA.
DR EMBL; AC006953; AAD17388.1; -; Genomic_DNA.
DR EMBL; AC006953; AAD17387.1; -; Genomic_DNA.
DR EMBL; BC002788; AAH02788.1; -; mRNA.
DR EMBL; AF257789; AAF71751.1; -; mRNA.
DR EMBL; S78532; AAD14289.1; -; Genomic_DNA.
DR EMBL; A18757; CAA01421.1; -; Unassigned_RNA.
DR PIR; I52614; I52614.
DR PIR; S39495; S39495.
DR Ensembl; ENSG00000011422; Homo sapiens.
DR HGNC; HGNC:9053; PLAUR.
DR H-InvDB; HIX0015192; -.
DR Reactome; Q03405; -.
DR MIM; 173391; -.
DR GO; GO:0009986; C:cell surface; IEP.
DR GO; GO:0019898; C:extrinsic to membrane; TAS.

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:13 ; Search time 20.544 Seconds
(without alignments)
1130.835 Million cell updates/sec

Title: US-10-679-951-2
Perfect score: 1583
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1546	97.7	335	1	US-08-085-122-13	Sequence 13, Appl
2	1546	97.7	335	2	US-08-442-108B-23	Sequence 23, Appl
3	1546	97.7	335	2	US-09-949-002-346	Sequence 346, App
4	1546	97.7	417	2	US-09-949-002-527	Sequence 527, App
5	515	32.5	90	1	US-08-085-122-5	Sequence 5, Appli
6	515	32.5	90	1	US-08-319-052-5	Sequence 5, Appli
7	515	32.5	90	2	US-08-442-108B-5	Sequence 5, Appli
8	448	28.3	92	1	US-08-085-122-3	Sequence 3, Appli
9	448	28.3	92	1	US-08-319-052-3	Sequence 3, Appli
10	448	28.3	92	2	US-08-442-108B-3	Sequence 3, Appli
11	344	21.7	99	1	US-08-085-122-4	Sequence 4, Appli
12	344	21.7	99	1	US-08-319-052-4	Sequence 4, Appli
13	344	21.7	99	2	US-08-442-108B-4	Sequence 4, Appli
14	183	11.6	34	1	US-08-085-122-11	Sequence 11, Appl
15	183	11.6	34	1	US-08-319-052-21	Sequence 21, Appl
16	183	11.6	34	2	US-08-442-108B-21	Sequence 21, Appl
17	147	9.3	204	1	US-08-652-859-2	Sequence 2, Appli
18	147	9.3	204	1	US-08-919-706-2	Sequence 2, Appli
19	147	9.3	204	1	US-09-153-751-2	Sequence 2, Appli
20	147	9.3	204	2	US-09-886-319A-38	Sequence 38, Appl
21	147	9.3	228	2	US-09-886-319A-45	Sequence 45, Appl
22	145.5	9.2	346	2	US-09-991-181-197	Sequence 197, App
23	145.5	9.2	346	2	US-09-990-444-197	Sequence 197, App
24	145.5	9.2	346	2	US-09-997-333-197	Sequence 197, App
25	145.5	9.2	346	2	US-09-992-598-197	Sequence 197, App
26	139.5	8.8	212	2	US-09-886-319A-37	Sequence 37, Appl
27	133.5	8.4	220	2	US-09-844-497-2	Sequence 2, Appli
28	133.5	8.4	220	2	US-10-404-170-2	Sequence 2, Appli
29	127	8.0	30	1	US-08-085-122-2	Sequence 2, Appli
30	127	8.0	30	1	US-08-319-052-2	Sequence 2, Appli
31	127	8.0	30	2	US-08-442-108B-2	Sequence 2, Appli
32	119.5	7.5	116	2	US-09-621-976-7212	Sequence 7212, Ap
33	119	7.5	735	2	US-09-191-647-9	Sequence 9, Appli
34	119	7.5	735	2	US-09-540-245A-9	Sequence 9, Appli
35	119	7.5	735	2	US-09-540-153-9	Sequence 9, Appli
36	119	7.5	735	2	US-10-289-776-9	Sequence 9, Appli
37	117	7.4	21	2	US-08-657-339A-11	Sequence 11, Appl
38	117	7.4	21	2	US-08-457-694A-11	Sequence 11, Appl
39	114.5	7.2	2556	1	US-08-185-432-17	Sequence 17, Appl
40	114.5	7.2	2556	2	US-08-899-232-2	Sequence 2, Appli
41	114.5	7.2	2556	2	US-09-121-457-2	Sequence 2, Appli
42	112.5	7.1	500	2	US-09-423-753-2	Sequence 2, Appli
43	112.5	7.1	659	2	US-09-423-753-3	Sequence 3, Appli
44	112.5	7.1	685	2	US-08-872-855-2	Sequence 2, Appli
45	112.5	7.1	685	2	US-09-423-753-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-085-122-13
; Sequence 13, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-085-122-13

Query Match 97.7%; Score 1546; DB 1; Length 335;
Best Local Similarity 83.9%; Pred. No. 7.1e-136;
Matches 281; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

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Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 -----------------------------------GRPKDDRHLRGCGYLPGCPGSNG 126
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Qy        127 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 186
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Qy        187 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 246
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RESULT 2
US-08-442-108B-23
; Sequence 23, Application US/08442108B
; Patent No. 6248712
;  GENERAL INFORMATION:
;    APPLICANT:  DANO, KELD
;    APPLICANT:  BLASI, FRANCESCO
;    APPLICANT:  ROLDAN, ANN LOURING
;    APPLICANT:  CUBELLIS, MARIA VITTORIA
;    APPLICANT:  MASUCCI, MARIA TERESA
;    APPLICANT:  APPELLA, ETTORE
;    APPLICANT:  SCHLEUNING, WOLF-DIETER
;    APPLICANT:  BEHRENDT, NIELS
;    APPLICANT:  KRISTENSEN, PETER
;    APPLICANT:  POLLANEN, JARI
;    APPLICANT:  SALONEN, EEVA-MARJATTA
;    TITLE OF INVENTION:  UROKINASE-TYPE PLASMINOGEN ACTIVATOR
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,108B
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/319,052
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/824,189
;      FILING DATE:  06-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/DK90/00090
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/374,854
;      FILING DATE:  03-JUL-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/334,613
;      FILING DATE:  07-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  DANO=1D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-442-108B-23

  Query Match             97.7%;  Score 1546;  DB 2;  Length 335;
  Best Local Similarity   83.9%;  Pred. No. 7.1e-136;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
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RESULT 3
US-09-949-002-346
; Sequence 346, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-346

  Query Match             97.7%;  Score 1546;  DB 2;  Length 335;
  Best Local Similarity   83.9%;  Pred. No. 7.1e-136;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:34 ; Search time 58.4981 Seconds
(without alignments)
2007.073 Million cell updates/sec

Title: US-10-679-951-2
Perfect score: 1583
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1583	100.0	281	4	US-10-679-951-9	Sequence 9, Appli
3	1546	97.7	335	4	US-10-193-656-6	Sequence 6, Appli
4	1546	97.7	335	4	US-10-177-293-362	Sequence 362, App
5	1546	97.7	335	4	US-10-295-027-1327	Sequence 1327, Ap
6	1546	97.7	335	4	US-10-429-160-75	Sequence 75, Appl
7	1546	97.7	335	4	US-10-679-951-8	Sequence 8, Appli
8	1546	97.7	335	5	US-10-783-528-97	Sequence 97, Appl
9	1546	97.7	335	5	US-10-723-860-2344	Sequence 2344, Ap
10	1546	97.7	335	5	US-10-482-029-160	Sequence 160, App
11	1353	85.5	301	4	US-10-755-889-424	Sequence 424, App
12	1298	82.0	289	4	US-10-679-951-11	Sequence 11, Appl
13	1293.5	81.7	290	4	US-10-679-951-6	Sequence 6, Appli
14	1271.5	80.3	236	4	US-10-679-951-4	Sequence 4, Appli
15	1268	80.1	235	4	US-10-679-951-10	Sequence 10, Appl
16	1263	79.8	287	4	US-10-087-192-1806	Sequence 1806, Ap
17	1259	79.5	283	5	US-10-993-007-1	Sequence 1, Appli
18	911	57.5	327	4	US-10-087-192-1803	Sequence 1803, Ap
19	515	32.5	90	3	US-09-755-109-5	Sequence 5, Appli
20	448	28.3	92	3	US-09-755-109-3	Sequence 3, Appli
21	344	21.7	99	3	US-09-755-109-4	Sequence 4, Appli
22	183	11.6	34	3	US-09-755-109-21	Sequence 21, Appl
23	150.5	9.5	366	5	US-10-450-763-45496	Sequence 45496, A
24	147	9.3	204	3	US-09-886-319A-38	Sequence 38, Appl
25	147	9.3	204	3	US-09-875-520-2	Sequence 2, Appli
26	147	9.3	204	4	US-10-376-564-38	Sequence 38, Appl
27	147	9.3	228	3	US-09-886-319A-45	Sequence 45, Appl
28	147	9.3	228	4	US-10-376-564-45	Sequence 45, Appl
29	145.5	9.2	346	3	US-09-989-722-197	Sequence 197, App
30	145.5	9.2	346	3	US-09-989-723-197	Sequence 197, App
31	145.5	9.2	346	3	US-09-989-279-197	Sequence 197, App
32	145.5	9.2	346	3	US-09-989-727-197	Sequence 197, App
33	145.5	9.2	346	3	US-09-989-731-197	Sequence 197, App
34	145.5	9.2	346	3	US-09-989-732-197	Sequence 197, App
35	145.5	9.2	346	3	US-09-991-073-197	Sequence 197, App
36	145.5	9.2	346	3	US-09-990-442-197	Sequence 197, App
37	145.5	9.2	346	3	US-09-991-163-197	Sequence 197, App
38	145.5	9.2	346	3	US-09-993-604-197	Sequence 197, App
39	145.5	9.2	346	3	US-09-990-456-197	Sequence 197, App
40	145.5	9.2	346	3	US-09-989-721-197	Sequence 197, App
41	145.5	9.2	346	3	US-09-992-598-197	Sequence 197, App
42	145.5	9.2	346	3	US-09-989-293A-197	Sequence 197, App
43	145.5	9.2	346	3	US-09-989-735-197	Sequence 197, App
44	145.5	9.2	346	3	US-09-990-444-197	Sequence 197, App
45	145.5	9.2	346	3	US-09-991-181-197	Sequence 197, App

ALIGNMENTS

RESULT 1
US-10-679-951-2
; Sequence 2, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-679-951-2

Query Match 100.0%; Score 1583; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-136;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 CPGSNGFHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFL 180
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Qy        241 HPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
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RESULT 2
US-10-679-951-9
; Sequence 9, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-679-951-9

  Query Match             100.0%;  Score 1583;  DB 4;  Length 281;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-136;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 6, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
;  APPLICANT: NY, Tor
;  APPLICANT:  HOLMDAHL, Rikard
;  APPLICANT:  LI, Jinan
;  TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
;  FILE REFERENCE: 3810/1J577-US3
;  CURRENT APPLICATION NUMBER: US/10/193,656
;  CURRENT FILING DATE:  2002-07-10
;  PRIOR APPLICATION NUMBER: US 60/304,461
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/304,490
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/305,182
;  PRIOR FILING DATE: 2001-07-13
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank / Q03405
;   DATABASE ENTRY DATE: 1994-02-01
;   RELEVANT RESIDUES: (1)..(335)
US-10-193-656-6

  Query Match             97.7%;  Score 1546;  DB 4;  Length 335;
  Best Local Similarity   83.9%;  Pred. No. 1.6e-132;
  Matches  281;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
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Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        127 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 186
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Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        187 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 246
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Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        247 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281
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Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 4
US-10-177-293-362
; Sequence 362, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Gannavarpu, Manjula
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Mertens, Maureen
;  APPLICANT:  Myer, Vic
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Monahan, John
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Bast Jr., Robert C.
;  APPLICANT:  Hortobagyi, Gabriel N.
;  APPLICANT:  Pusztai, Lajos
;  APPLICANT:  Meric, Funda
;  APPLICANT:  Sahin, Aysegul
;  APPLICANT:  Mills, Gordon B.
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
;  TITLE OF INVENTION:  PREVENTION, AND THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-038
;  CURRENT APPLICATION NUMBER: US/10/177,293
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,887
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/301,572
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 1583
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	145.5	9.2	346	6	US-10-131-826A-432	Sequence 432, App
2	145.5	9.2	346	6	US-10-967-457-77	Sequence 77, Appl
3	123.5	7.8	1418	6	US-10-453-372-864	Sequence 864, App
4	118.5	7.5	1574	6	US-10-055-877-211	Sequence 211, App
5	112.5	7.1	685	6	US-10-131-826A-88	Sequence 88, Appl
6	112.5	7.1	685	7	US-11-078-735-19	Sequence 19, Appl
7	112.5	7.1	685	7	US-11-050-346-64	Sequence 64, Appl
8	112.5	7.1	685	7	US-11-103-077-19	Sequence 19, Appl
9	112.5	7.1	1198	6	US-10-453-372-880	Sequence 880, App
10	112.5	7.1	1398	6	US-10-055-877-46	Sequence 46, Appl
11	112.5	7.1	1398	6	US-10-453-372-872	Sequence 872, App
12	112.5	7.1	1450	6	US-10-055-877-48	Sequence 48, Appl
13	112.5	7.1	1450	6	US-10-453-372-874	Sequence 874, App
14	112.5	7.1	1594	6	US-10-453-372-860	Sequence 860, App
15	111.5	7.0	1403	6	US-10-055-877-52	Sequence 52, Appl
16	111.5	7.0	1403	6	US-10-453-372-878	Sequence 878, App
17	111.5	7.0	1404	6	US-10-055-877-44	Sequence 44, Appl
18	111.5	7.0	1404	6	US-10-453-372-870	Sequence 870, App
19	111.5	7.0	1547	6	US-10-453-372-886	Sequence 886, App
20	111.5	7.0	1577	6	US-10-055-877-54	Sequence 54, Appl
21	111.5	7.0	1577	6	US-10-453-372-882	Sequence 882, App
22	111.5	7.0	1577	6	US-10-453-372-884	Sequence 884, App
23	111.5	7.0	1620	6	US-10-453-372-868	Sequence 868, App
24	111.5	7.0	1653	6	US-10-453-372-866	Sequence 866, App
25	111.5	7.0	3333	6	US-10-766-317-4	Sequence 4, Appli
26	110	6.9	3002	6	US-10-821-234-916	Sequence 916, App
27	108.5	6.9	1620	6	US-10-055-877-213	Sequence 213, App
28	108	6.8	1140	6	US-10-055-877-215	Sequence 215, App
29	107.5	6.8	2556	7	US-11-050-346-67	Sequence 67, Appl
30	107	6.8	712	6	US-10-995-561-984	Sequence 984, App
31	107	6.8	769	6	US-10-995-561-985	Sequence 985, App
32	107	6.8	769	6	US-10-995-561-986	Sequence 986, App
33	107	6.8	769	7	US-11-107-028-5	Sequence 5, Appli
34	107	6.8	997	7	US-11-113-424-37	Sequence 37, Appl
35	103.5	6.5	969	6	US-10-055-877-214	Sequence 214, App
36	102	6.4	961	7	US-11-113-424-35	Sequence 35, Appl
37	102	6.4	1664	6	US-10-055-877-212	Sequence 212, App
38	101.5	6.4	915	6	US-10-131-826A-294	Sequence 294, App
39	100	6.3	703	6	US-10-821-234-1412	Sequence 1412, Ap
40	100	6.3	816	7	US-11-090-439-48	Sequence 48, Appl
41	100	6.3	956	7	US-11-113-424-39	Sequence 39, Appl
42	99.5	6.3	2471	7	US-11-050-346-68	Sequence 68, Appl
43	98.5	6.2	1416	7	US-11-128-059-60	Sequence 60, Appl
44	98.5	6.2	1494	7	US-11-128-059-78	Sequence 78, Appl
45	98.5	6.2	2086	7	US-11-128-059-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-10-131-826A-432
; Sequence 432, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.

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;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 432
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-432

  Query Match             9.2%;  Score 145.5;  DB 6;  Length 346;
  Best Local Similarity   24.2%;  Pred. No. 1.5e-06;
  Matches   71;  Conservative   22;  Mismatches  113;  Indels   87;  Gaps   14;

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Qy         62 LVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPGC 121
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Db         67 AVE-----------TIHGQFSLAV--------------------------RGCG--SGL 86

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Qy        222 DAFSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHLSLTITLLMT 270
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; Sequence 77, Application US/10967457
; Publication No. US20050244931A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF545PCT
;  CURRENT APPLICATION NUMBER: US/10/967,457
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: US/09/833,041
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/229,358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256,931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199,384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-967-457-77

  Query Match             9.2%;  Score 145.5;  DB 6;  Length 346;
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  Matches   71;  Conservative   22;  Mismatches  113;  Indels   87;  Gaps   14;

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Qy         62 LVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPGC 121
               ||           |:  :  | :                                ||||   |
Db         67 AVE-----------TIHGQFSLAV--------------------------RGCG--SGL 86

Qy        122 PGSN----GFHNNDTFHFLKCCNTTKCNE---------GPILELENLPQNGRQCYSCKGN 168
              || |     |    |  |: |   :||            |        | || :|||| |
Db         87 PGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRALDPAGNESAYPPNGVECYSCVGL 146

Qy        169 STHGCSSEETFLIDCRGPMNQ----CLVATGTHEPKN--QSYMVRGCATASMC-QHAHLG 221
              |   |      :: |    :      |      |    |   | ||||     | :    |
Db        147 SREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTVSLPVRGCVQDEFCTRDGVTG 206

Qy        222 DAFSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHLSLTITLLMT 270
                |:::    |||  | ||    :  | |   |      | |   ::  |  :|
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RESULT 3
US-10-453-372-864
; Sequence 864, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-589 A
;  CURRENT APPLICATION NUMBER: US/10/453,372
;  CURRENT FILING DATE:  2003-06-03
;  PRIOR APPLICATION NUMBER: 09/789390
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 09/823187
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/195792
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 09/839446
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/199476
;  PRIOR FILING DATE: 2000-03-25
;  PRIOR APPLICATION NUMBER: 09/863776
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 60/208263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 09/939398
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/227800
;  PRIOR FILING DATE: 2000-08-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1609
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 864
;   LENGTH: 1418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-453-372-864

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  Best Local Similarity   21.1%;  Pred. No. 0.00081;
  Matches   64;  Conservative   29;  Mismatches  107;  Indels  103;  Gaps   17;

Qy         16 CVPASWGLRCM----QCKT-NGDCR----------------------------VEECAL 41
              | |   | ||     :|:| || |:                           :  |||
Db        153 CPPGFQGPRCQYDVDECRTHNGGCQHRCVNTPGSYLCECKPGFRLHTDSRTCLAINSCAL 212

Qy         42 GQDLCRTTIVRL--------WEEGEELELVEKSCTHSE---KTNRTLSYRTGLKITSLTE 90
              |   |:   |:|           | :|:   : |          | :  :|  : :  |
Db        213 GNGGCQHHCVQLTITRHRCQCRPGFQLQEDGRHCVRRSPCANRNGSCMHRCQV-VRGLAR 271

Qy         91 VVC--GLDLCNQGNSGRPKDD--RHLRGCGYLPGCPGSNGFHNNDTFHFLKCCNTTKCNE 146
              |  |  |   | :    |:    |  | :  ||  : |          ||     |:
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Qy        147 GPILELENLPQNGRQCY--------SCKGNS---THGCSSEETFLIDCRGPMNQCLVATG 195
              |       | :|||||         ||: |:   :||||          ||:  |
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:07:51 ; Search time 3686.08 Seconds
(without alignments)
10964.406 Million cell updates/sec

Title: US-10-679-951-3
Perfect score: 711
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb_pat:*
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8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	6	AX663344	AX663344 Sequence
2	566	79.6	846	6	AX663342	AX663342 Sequence
3	539	75.8	873	6	AX663346	AX663346 Sequence
4	539	75.8	1608	8	HSU08839	U08839 Human uroki
5	502.8	70.7	1609	6	AX281707	AX281707 Sequence
6	404	56.8	1008	6	AX663348	AX663348 Sequence
7	404	56.8	1008	11	AY893435	AY893435 Synthetic
8	404	56.8	1318	6	AX481417	AX481417 Sequence
9	404	56.8	1349	6	AR380630	AR380630 Sequence
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11	404	56.8	1353	8	BC002788	BC002788 Homo sapi
12	404	56.8	1363	6	AX787055	AX787055 Sequence
13	404	56.8	1363	8	HSUPARAA	X51675 H.sapiens u
14	404	56.8	1400	6	A18757	A18757 u-PA recept
15	404	56.8	1400	6	BD140440	BD140440 Urokinase
16	404	56.8	1400	6	BD188995	BD188995 Antibodie
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28	400.4	56.3	1008	11	BT019742	BT019742 Synthetic
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33	377.2	53.1	1046	8	AF302072	AF302072 Cercopith
34	375.6	52.8	1067	8	AF302073	AF302073 Macaca fa
35	358.2	50.4	967	8	AF257789	AF257789 Homo sapi
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45	257.2	36.2	1335	4	S70635	S70635 urokinase-t

ALIGNMENTS

RESULT 1
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LOCUS AX663344 711 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3 from Patent WO02082077.
ACCESSION AX663344
VERSION AX663344.1 GI:29163686
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
TITLE Production of polyclonal monospecific antibodies against upar variants del4, del5 and del4+5, and the use thereof for diagnostic and therapeutical purposes
JOURNAL Patent: WO 02082077-A 3 17-OCT-2002;
Wilex AG (DE)
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ORIGIN

Query Match 100.0%; Score 711; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 1.8e-182;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
Db        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
Db        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240

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Qy        541 ATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGAT 600
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Qy        601 GTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATC 660
Db        601 GTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATC 660

Qy        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711
Db        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711


RESULT 2
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LOCUS       AX663342                846 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 1 from Patent WO02082077.
ACCESSION   AX663342
VERSION     AX663342.1  GI:29163684
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
  TITLE     Production of polyclonal monospecific antibodies against upar
            variants del4, del5 and del4+5, and the use thereof for diagnostic
            and therapeutical purposes
  JOURNAL   Patent: WO 02082077-A 1 17-OCT-2002;
            Wilex AG (DE)
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                     TLLWT"
ORIGIN

  Query Match             79.6%;  Score 566;  DB 6;  Length 846;
  Best Local Similarity   84.0%;  Pred. No. 5.8e-143;
  Matches  711;  Conservative    0;  Mismatches    0;  Indels  135;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
Db          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
Db         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
Db        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Qy        301 GGCAACTCTG---------------------------------------------------- 310
Db        301 GGCAACTCTGGGCGTCCAAAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGC 360

Qy        311 ---------------------------------------------------------- 310
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Qy        311 -------------------------TCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGC 345
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Qy        346 CAGTGTTACAGCTGCAAGGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTC 405
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Qy        406 ATTGACTGCCGAGGCCCCATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAA 465
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Qy        526 GGTGACGCCTTCAGCATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAAC 585
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Qy        586 CACCCAGACCTGGATGTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCAT 645
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Qy        706 ACCTAA 711
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:05:06 ; Search time 436.548 Seconds
(without alignments)
10854.694 Million cell updates/sec

Title: US-10-679-951-3
Perfect score: 711
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	9	ABZ26097	Abz26097 Human uPA
2	566	79.6	846	9	ABZ26096	Abz26096 Human uPA
3	539	75.8	873	9	ABZ26098	Abz26098 Human uPA
c 4	539	75.8	1608	10	ABZ82961	Abz82961 Toxicolog
5	511	71.9	1601	11	ACN45051	Acn45051 Human mRN
6	502.8	70.7	1609	6	AAS94861	Aas94861 Human DNA
7	404	56.8	1008	9	ABZ26099	Abz26099 Human uPA
8	404	56.8	1318	6	ABV78147	Abv78147 Human uro
9	404	56.8	1318	6	ABZ35723	Abz35723 Human UPA
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14	404	56.8	1363	10	AAD56134	Aad56134 Human uro
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16	404	56.8	1400	2	AAT29191	Aat29191 Human uro
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44	396.4	55.8	1400	2	ACA62905	Aca62905 cDNA enco
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ALIGNMENTS

RESULT 1
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ID ABZ26097 standard; cDNA; 711 BP.
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AC ABZ26097;
XX
DT 27-MAR-2003 (first entry)
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DE Human uPAR exon 4 & 5 deletion variant encoding cDNA SEQ ID NO 3.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; gene; ss.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN DE10117381-A1.
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PD 10-OCT-2002.
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PF 06-APR-2001; 2001DE-01017381.
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PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR P-PSDB; ABP60420.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 2; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a

```
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 4 and 5 deletion variant encoding
CC   cDNA of the invention
XX
SQ   Sequence 711 BP; 161 A; 211 C; 198 G; 141 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 711;  DB 9;  Length 711;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-185;
  Matches  711;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Qy        301 GGCAACTCTGTCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGC 360
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Db        301 GGCAACTCTGTCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGC 360

Qy        361 AAGGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGC 420
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Db        361 AAGGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGC 420

Qy        421 CCCATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATG 480
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Qy        481 GTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGC 540
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Qy        541 ATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGAT 600
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Qy        601 GTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATC 660
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Qy        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711
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Db        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711


RESULT 2
ABZ26096
ID   ABZ26096 standard; cDNA; 846 BP.
XX
AC   ABZ26096;
XX
DT   27-MAR-2003  (first entry)
XX
DE   Human uPAR exon 4 deletion variant encoding cDNA SEQ ID NO 1.
XX
KW   Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW   cancer; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .846
FT                   /*tag= a
FT                   /product= "uPAR exon 4 deletion variant"
XX
PN   DE10117381-A1.
XX
PD   10-OCT-2002.
XX
PF   06-APR-2001; 2001DE-01017381.
XX
PR   06-APR-2001; 2001DE-01017381.
XX
PA   (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI   Luther T,  Magdolen V,  Schmitt M,  Muehlenweg B;
XX
DR   WPI; 2003-168688/17.
DR   P-PSDB; ABP60419.
XX
PT   New nucleic acid encoding a deletion variant of a urokinase receptor
PT   which has one of two exons missing, is useful to detect and treat cancer,
PT   particularly breast and ovarian cancer.
XX
PS   Disclosure; Fig 1; 28pp; German.
XX
CC   The invention relates to a nucleic acid encoding a deletion variant of a
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 4 deletion variant encoding cDNA
CC   of the invention
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SQ   Sequence 846 BP; 193 A; 261 C; 228 G; 164 T; 0 U; 0 Other;

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  Best Local Similarity  84.0%;  Pred. No. 1.2e-145;
  Matches  711;  Conservative    0;  Mismatches    0;  Indels  135;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Db        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Qy        301 GGCAACTCTG---------------------------------------------------- 310
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Db        301 GGCAACTCTGGGCGTCCAAAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGC 360

Qy        311 ---------------------------------------------------------- 310

Db        361 TGCCCGGGCTCCAATGGTTTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAAC 420

Qy        311 -------------------------TCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGC 345
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:10:21 ; Search time 2877.06 Seconds
(without alignments)
11562.352 Million cell updates/sec

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Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_est3:*
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11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	404	56.8	1008	11	DQ050301	DQ050301 Homo sapi
	3	404	56.8	1303	4	CR606767	CR606767 full-leng
	4	404	56.8	1320	4	CR611518	CR611518 full-leng
	5	404	56.8	1348	4	CR591481	CR591481 full-leng
	6	403	56.7	905	3	BI906745	BI906745 603064474
	7	401.2	56.4	492	3	BI793227	BI793227 ie49e04.y
	8	401.2	56.4	501	7	CK821016	CK821016 ie47g09.y
	9	401.2	56.4	502	3	BI793096	BI793096 ie47g09.y
	10	401.2	56.4	560	6	CB158636	CB158636 K-EST0218
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	12	401.2	56.4	1724	4	CR601067	CR601067 full-leng
c	13	400.2	56.3	718	6	CD367492	CD367492 UI-H-FT1-
c	14	400.2	56.3	744	6	CD368062	CD368062 UI-H-FT1-
c	15	400.2	56.3	759	5	BU687998	BU687998 UI-CF-EC1
c	16	399.2	56.1	736	5	BU608773	BU608773 UI-CF-FN0
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c	18	398.6	56.1	749	6	CB305662	CB305662 UI-CF-EN1
	19	398.2	56.0	449	6	CB144030	CB144030 K-EST0198
c	20	398	56.0	532	2	BF736997	BF736997 PM4-KT004
c	21	398	56.0	735	5	BU634064	BU634064 UI-H-FL1-
c	22	397.6	55.9	750	5	BU626444	BU626444 UI-H-FT0-
c	23	397	55.8	408	1	AW351505	AW351505 IL2-CT003
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c	27	390.4	54.9	501	1	AW392589	AW392589 PM4-ST026
c	28	388.4	54.6	971	1	AL577205	AL577205 AL577205
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c	31	384.2	54.0	717	3	BQ008722	BQ008722 UI-H-EI0-
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ALIGNMENTS

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LOCUS BM543893 1078 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6492429 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589238 5', mRNA sequence.
ACCESSION BM543893
VERSION BM543893.1 GI:18774681
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12361 row: j column: 23
High quality sequence start: 29
High quality sequence stop: 601.
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 036."

ORIGIN

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  Query Match             65.9%;  Score 468.2;  DB 3;  Length 1078;
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  Matches  676;  Conservative    0;  Mismatches   25;  Indels  164;  Gaps    3;

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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        301 GGCAACTCT---------------------------------------------------- 309
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Db        343 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 402

Qy        310 ---------------------------------------------------------- 309

Db        403 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 462

Qy        310 ----------------------------------------------------GTCCTGGAG 318
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Qy        319 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 378
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Qy        379 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 438
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Qy        499 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 558
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RESULT 2
DQ050301
LOCUS DQ050301 1008 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens PLAUR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ050301
VERSION DQ050301.1 GI:66903500
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

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ORIGIN

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Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        311 ---------------------------------------------------------- 310

Db        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGGGCGTCCA 480
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:24:01 ; Search time 143.956 Seconds
(without alignments)
8779.420 Million cell updates/sec

Title: US-10-679-951-3
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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	404	56.8	1400	2	US-08-085-122-12	Sequence 12, Appl
	3	404	56.8	1400	3	US-08-442-108B-22	Sequence 22, Appl
	4	404	56.8	1743	3	US-09-949-002-60	Sequence 60, Appl
	5	404	56.8	1745	3	US-09-949-002-241	Sequence 241, App
	6	255	35.9	25966	3	US-09-949-002-632	Sequence 632, App
	7	255	35.9	25966	3	US-09-949-002-813	Sequence 813, App
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c	10	84.8	11.9	601	3	US-09-949-002-2317	Sequence 2317, Ap
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	15	43.6	6.1	1527	3	US-09-489-039A-716	Sequence 716, App
c	16	42	5.9	56	3	US-09-381-244B-24	Sequence 24, Appl
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	18	39.4	5.5	7847	3	US-09-799-451-591	Sequence 591, App
c	19	38	5.3	116955	3	US-09-949-016-17565	Sequence 17565, A
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c	26	37.2	5.2	2887	3	US-09-964-899-34	Sequence 34, Appl
c	27	37.2	5.2	2977	3	US-09-919-039-65	Sequence 65, Appl
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	31	36.8	5.2	4843	3	US-09-402-923A-2	Sequence 2, Appli
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	33	36.8	5.2	5098	3	US-09-402-923A-1	Sequence 1, Appli
	34	36.8	5.2	5103	3	US-09-949-016-2457	Sequence 2457, Ap
	35	36.8	5.2	5120	3	US-09-544-398B-1	Sequence 1, Appli
	36	36.8	5.2	5120	3	US-09-544-398B-2	Sequence 2, Appli
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	38	36.8	5.2	5120	3	US-09-543-771B-2	Sequence 2, Appli
	39	36.6	5.1	1296	3	US-09-489-039A-1107	Sequence 1107, Ap
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	41	36	5.1	36	2	US-08-319-052-6	Sequence 6, Appli
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	43	36	5.1	1068	3	US-09-489-039A-5954	Sequence 5954, Ap
	44	36	5.1	1089	3	US-09-195-666A-10	Sequence 10, Appl
	45	36	5.1	1089	3	US-09-635-705-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-023-655-1175
; Sequence 1175, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g188623

US-09-023-655-1175

Query Match 56.8%; Score 404; DB 3; Length 1349;
Best Local Similarity 70.5%; Pred. No. 1.1e-108;
Matches 711; Conservative 0; Mismatches 0; Indels 297; Gaps 1;

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; Sequence 12, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..1054
US-08-085-122-12

Query Match 56.8%; Score 404; DB 2; Length 1400;
Best Local Similarity 70.5%; Pred. No. 1.1e-108;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:30:50 ; Search time 654.53 Seconds
(without alignments)
8982.829 Million cell updates/sec

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Perfect score: 711
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	539	75.8	873	8	US-10-679-951-5	Sequence 5, Appli
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7	404	56.8	1318	7	US-10-384-339C-31	Sequence 31, Appl
8	404	56.8	1349	7	US-10-641-643-1175	Sequence 1175, Ap
9	404	56.8	1363	5	US-10-193-656-5	Sequence 5, Appli
10	404	56.8	1740	8	US-10-783-528-39	Sequence 39, Appl
11	404	56.8	1743	6	US-10-177-293-361	Sequence 361, App
12	404	56.8	1743	6	US-10-172-118-799	Sequence 799, App
13	404	56.8	1743	6	US-10-388-360-372	Sequence 372, App
14	404	56.8	1743	6	US-10-295-027-1110	Sequence 1110, Ap
15	404	56.8	1743	7	US-10-429-160-74	Sequence 74, Appl
16	404	56.8	1743	7	US-10-342-887-799	Sequence 799, App
17	404	56.8	1743	8	US-10-723-860-2343	Sequence 2343, Ap
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19	404	56.8	1887	8	US-10-723-860-6539	Sequence 6539, Ap
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22	312.8	44.0	483	3	US-09-919-580-200	Sequence 200, App
23	312.8	44.0	952	7	US-10-755-889-423	Sequence 423, App
24	312.8	44.0	1097	7	US-10-240-425-1547	Sequence 1547, Ap
25	312.8	44.0	1097	7	US-10-717-597-101	Sequence 101, App
26	255	35.9	739	3	US-09-962-832-120	Sequence 120, App
27	255	35.9	739	8	US-10-482-029-159	Sequence 159, App
28	255	35.9	739	9	US-10-843-641A-6006	Sequence 6006, Ap
29	255	35.9	41966	5	US-10-087-192-1804	Sequence 1804, Ap
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c 32	148.8	20.9	521	6	US-10-029-386-7358	Sequence 7358, Ap
c 33	147	20.7	148	6	US-10-029-386-21058	Sequence 21058, A
34	143.6	20.2	409	3	US-09-813-358-205	Sequence 205, App
35	143.6	20.2	409	3	US-09-997-279-205	Sequence 205, App
c 36	117	16.5	561	6	US-10-029-386-11796	Sequence 11796, A
c 37	111	15.6	112	6	US-10-029-386-25496	Sequence 25496, A
38	104	14.6	406	5	US-10-066-543-1724	Sequence 1724, Ap
39	104	14.6	406	5	US-10-066-543-2399	Sequence 2399, Ap
40	99.8	14.0	431	8	US-10-357-930-37459	Sequence 37459, A
41	86.6	12.2	32963	5	US-10-087-192-1801	Sequence 1801, Ap
42	86.4	12.2	275	8	US-10-357-930-7499	Sequence 7499, Ap
43	76	10.7	76	8	US-10-714-195-72	Sequence 72, Appl
44	76	10.7	76	9	US-10-852-797-352	Sequence 352, App
45	50.2	7.1	289	3	US-09-783-590-12057	Sequence 12057, A

ALIGNMENTS

RESULT 1
US-10-679-951-3
; Sequence 3, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnostic
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-679-951-3

Query Match 100.0%; Score 711; DB 8; Length 711;
Best Local Similarity 100.0%; Pred. No. 2.6e-216;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        481 GTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGC 540
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Db        481 GTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGC 540

Qy        541 ATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGAT 600

Qy        601 GTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATC 660
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Qy        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711
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Db        661 ACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711


RESULT 2
US-10-679-951-1
; Sequence 1, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-679-951-1

  Query Match             79.6%;  Score 566;  DB 8;  Length 846;
  Best Local Similarity   84.0%;  Pred. No. 5.7e-170;
  Matches  711;  Conservative    0;  Mismatches    0;  Indels  135;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        301 GGCAACTCTG---------------------------------------------------- 310
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Qy        311 ---------------------------------------------------------- 310

Db        361 TGCCCGGGCTCCAATGGTTTCCACAACAACGACACCTTCCACTTCCTGAAATGCTGCAAC 420

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Qy        346 CAGTGTTACAGCTGCAAGGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTC 405
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Qy        406 ATTGACTGCCGAGGCCCCATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAA 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        466 AACCAAAGCTATATGGTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTG 525
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Db        601 AACCAAAGCTATATGGTAAGAGGCTGTGCAACCGCCTCAATGTGCCAACATGCCCACCTG 660

Qy        526 GGTGACGCCTTCAGCATGAACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAAC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        586 CACCCAGACCTGGATGTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCAT 645
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Db        721 CACCCAGACCTGGATGTCCAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCAT 780

Qy        646 CTCAGCCTCACCATCACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGG 705
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Db        781 CTCAGCCTCACCATCACCCTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGG 840

Qy        706 ACCTAA 711
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Db        841 ACCTAA 846


RESULT 3
US-10-679-951-5
; Sequence 5, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:56:22 ; Search time 312.489 Seconds
(without alignments)
1875.453 Million cell updates/sec

Title: US-10-679-951-3
Perfect score: 711
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	404	56.8	1743	6	US-10-826-585-57	Sequence 57, Appl
	2	171.2	24.1	600	8	US-11-128-061-4364	Sequence 4364, Ap
	3	171.2	24.1	600	8	US-11-128-049-4364	Sequence 4364, Ap
	4	171.2	24.1	972	8	US-11-128-061-722	Sequence 722, App
	5	171.2	24.1	972	8	US-11-128-049-722	Sequence 722, App
	6	164.6	23.2	1277	8	US-11-136-527-2432	Sequence 2432, Ap
	7	122.4	17.2	600	8	US-11-136-527-6528	Sequence 6528, Ap
	8	39.6	5.6	1506	7	US-10-971-560-9	Sequence 9, Appli
	9	39.6	5.6	3289	7	US-10-971-560-8	Sequence 8, Appli
	10	39.6	5.6	4158	7	US-10-971-560-3	Sequence 3, Appli
	11	39.6	5.6	6458	7	US-10-971-560-1	Sequence 1, Appli
	12	36.8	5.2	5100	8	US-11-108-528-79	Sequence 79, Appl
	13	34	4.8	649	7	US-10-516-768-7	Sequence 7, Appli
	14	33.6	4.7	3703	7	US-10-750-185-27363	Sequence 27363, A
	15	33.6	4.7	3703	7	US-10-750-623-27363	Sequence 27363, A
	16	33.6	4.7	5119	8	US-11-108-528-81	Sequence 81, Appl
	17	33.4	4.7	1625	7	US-10-750-185-43394	Sequence 43394, A
	18	33.4	4.7	1625	7	US-10-750-623-43394	Sequence 43394, A
c	19	33	4.6	1662	8	US-11-136-619-3	Sequence 3, Appli
c	20	32.6	4.6	1332	7	US-10-967-648A-7	Sequence 7, Appli
	21	32.6	4.6	157224	8	US-11-112-908-51	Sequence 51, Appl
	22	32.6	4.6	161726	8	US-11-112-908-48	Sequence 48, Appl
	23	32.6	4.6	161726	8	US-11-112-908-52	Sequence 52, Appl
	24	32.6	4.6	170189	8	US-11-112-908-50	Sequence 50, Appl
c	25	32.4	4.6	1684	7	US-10-750-185-29991	Sequence 29991, A
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c	27	32.2	4.5	1305	7	US-10-750-185-61512	Sequence 61512, A
c	28	32.2	4.5	1305	7	US-10-750-623-61512	Sequence 61512, A
c	29	32	4.5	951	7	US-10-750-185-32051	Sequence 32051, A
c	30	32	4.5	951	7	US-10-750-623-32051	Sequence 32051, A
	31	32	4.5	4564	7	US-10-750-185-63324	Sequence 63324, A
	32	32	4.5	4564	7	US-10-750-623-63324	Sequence 63324, A
	33	31.8	4.5	2989	8	US-11-136-527-3024	Sequence 3024, Ap
	34	31.8	4.5	5614	8	US-11-136-527-3578	Sequence 3578, Ap
c	35	31.8	4.5	19675	8	US-11-124-368A-2878	Sequence 2878, Ap
	36	31.6	4.4	2214	8	US-11-000-688-670	Sequence 670, App
	37	31.6	4.4	110847	8	US-11-121-086-11	Sequence 11, Appl
	38	31.2	4.4	1521	8	US-11-129-442-22	Sequence 22, Appl
	39	31.2	4.4	1595	8	US-11-108-528-23	Sequence 23, Appl
c	40	31.2	4.4	1885	7	US-10-750-185-29907	Sequence 29907, A
c	41	31.2	4.4	1885	7	US-10-750-623-29907	Sequence 29907, A
	42	31.2	4.4	184000	8	US-11-121-086-37	Sequence 37, Appl
	43	31.2	4.4	1691140	8	US-11-091-018-1	Sequence 1, Appli
	44	31	4.4	723	8	US-11-000-688-1560	Sequence 1560, Ap
	45	31	4.4	2516	8	US-11-186-284-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-10-826-585-57
; Sequence 57, Application US/10826585
; Publication No. US20060008807A1
; GENERAL INFORMATION:
; APPLICANT: Immunivest Corporation
; APPLICANT: O'Hara, Shawn Mark
; APPLICANT: Foulk, Brad
; APPLICANT: Zweitzig, Daniel
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
; TITLE OF INVENTION: morphological features on the same sample
; FILE REFERENCE: IMMC 143 PCT/US
; CURRENT APPLICATION NUMBER: US/10/826,585
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/369945
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/330669
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/26867
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Human
US-10-826-585-57

Query Match 56.8%; Score 404; DB 6; Length 1743;
Best Local Similarity 70.5%; Pred. No. 4.8e-104;
Matches 711; Conservative 0; Mismatches 0; Indels 297; Gaps 1;

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Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Db        427 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 486

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Db        487 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 546

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Db        667 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 726

Qy        301 GGCAACTCTG---------------------------------------------------- 310
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Db        727 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 786

Qy        311 ------------------------------------------------------------ 310

Db        787 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 846

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Qy        311 -------TCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 363
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Db       1027 GGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 1086

Qy        364 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 423
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Db       1087 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 1146

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Db       1147 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 1206

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Qy        544 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 603
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Db       1327 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 1386

Qy        664 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 711
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Db       1387 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1434
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RESULT 2
US-11-128-061-4364
; Sequence 4364, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4364
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-4364

Query Match 24.1%; Score 171.2; DB 8; Length 600;
Best Local Similarity 66.3%; Pred. No. 1.3e-38;
Matches 273; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

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Db        210 CAATGGCGGCCCAGTTCTAAATCTTCGGGACTTACCACCGAATGGCGTCCAGTGTTACAG 269

Qy        357 CTGCAAGGGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCG 416
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Db        270 CTGCGAGGGCAACAGCACCCACGGGTGTTCCTCCAAAGAGACTTCCCTCGTTGACTGCCG 329

Qy        417 AGGCCCCATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTA 476
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Db        330 GGGACCGATGGATCAGTGCCTGGAGGCCACCGGCTTGGATGTGCTGGCAAACCGGAGTCA 389

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; Sequence 4364, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4364
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-049-4364

Query Match 24.1%; Score 171.2; DB 8; Length 600;

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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:03 ; Search time 62.29 Seconds
(without alignments)
1664.689 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1305	100.0	236	6	ABP60420	Abp60420 Human uPA
2	1271.5	97.4	281	6	ABP60419	Abp60419 Human uPA
3	1268	97.2	290	6	ABP60421	Abp60421 Human uPA
4	1244.5	95.4	335	1	AAP60436	Aap60436 Sequence
5	1244.5	95.4	335	2	AAR07561	Aar07561 Recombina
6	1244.5	95.4	335	2	AAR44424	Aar44424 Human pho
7	1244.5	95.4	335	2	AAR58707	Aar58707 Human pho
8	1244.5	95.4	335	2	AAR97612	Aar97612 Human uro
9	1244.5	95.4	335	2	AAW31165	Aaw31165 Human pho
10	1244.5	95.4	335	4	AAU04454	Aau04454 Human uro
11	1244.5	95.4	335	6	AAE37129	Aae37129 Human uro
12	1244.5	95.4	335	6	ABR47562	Breast ca
13	1244.5	95.4	335	6	ABP60422	Abp60422 Human uPA
14	1244.5	95.4	335	7	ADN40009	Adn40009 Cancer/an
15	1244.5	95.4	335	8	ADJ45544	LXR-ligan
16	1244.5	95.4	335	8	ADO47984	Ado47984 Human uro
17	1244.5	95.4	335	8	ADP12460	Adp12460 Protein e
18	1244.5	95.4	335	8	ADQ19525	Human sof
19	1244.5	95.4	335	8	ADP24414	Adp24414 PRO polyp
20	1244.5	95.4	335	8	ADR46684	Adr46684 Cancer-as
21	1239.5	95.0	335	2	ABU10413	Abu10413 Human uro
22	1237.5	94.8	287	7	ABM85797	Abm85797 Human pro
23	1237.5	94.8	335	2	AAY04103	Aay04103 Urokinase
24	1233.5	94.5	335	4	AAU07610	Aau07610 Human u-P
25	1231.5	94.4	335	3	AAB26241	Aab26241 Human uro
26	1215.5	93.1	330	9	AEB54709	Aeb54709 Human pla
27	1171.5	89.8	359	6	ABU11701	Abu11701 Human MDD
28	1061.5	81.3	301	8	ADR14423	Adr14423 Human NF-
29	1052.5	80.7	299	4	AAU07611	Aau07611 Human u-P
30	1033	79.2	286	8	ABM84629	Abm84629 Human dia
31	957.5	73.4	283	8	ADU73621	Adu73621 Urokinase
32	957.5	73.4	283	9	AEA35322	Aea35322 Human mat
33	782.5	60.0	281	6	ABU89746	Abu89746 Protein d
34	757.5	58.0	174	1	AAP60435	Aap60435 Sequence
35	757.5	58.0	174	2	AAR44423	Aar44423 Peptide c
36	757.5	58.0	174	2	AAR58710	Aar58710 Human PIP
37	757.5	58.0	174	2	AAW31168	Aaw31168 hPIP part
38	704.5	54.0	327	7	ABM85796	Abm85796 Mouse pro
39	515	39.5	90	2	ABU10417	Abu10417 Human uro
40	515	39.5	90	2	AAY04101	Aay04101 Urokinase
41	515	39.5	90	4	AAU04458	Aau04458 Human u-P
42	437	33.5	92	2	AAW99896	Aaw99896 Urokinase
43	437	33.5	92	4	AAU04456	Aau04456 Human u-P
44	429	32.9	92	2	ABU10415	Abu10415 Human uro
45	295.5	22.6	94	1	AAP60434	Aap60434 Sequence

ALIGNMENTS

RESULT 1
ABP60420
ID ABP60420 standard; protein; 236 AA.
XX
AC ABP60420;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human uPAR exon 4 & 5 deletion variant protein SEQ ID NO 4.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; receptor.
XX
OS Homo sapiens.
XX
PN DE10117381-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001DE-01017381.
XX
PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR N-PSDB; ABZ26097.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 2; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a
CC urokinase type plasminogen activator receptor (uPAR) which has one or two
CC exons of the native sequence at least partly missing, excluding Genbank
CC sequence U08839. Molecules of the invention are used to diagnose,
CC prognose and treat cancer, particularly breast or ovarian cancer. The
CC present sequence is that of a uPAR exon 4 and 5 deletion variant protein
CC of the invention
XX
SQ Sequence 236 AA;

Query Match 100.0%; Score 1305; DB 6; Length 236;

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  Best Local Similarity   100.0%;  Pred. No. 6.6e-98;
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Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSVLELENLPQNGRQCYSC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSVLELENLPQNGRQCYSC 120

Qy        121 KGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFS 180

Qy        181 MNHIDVSCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MNHIDVSCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236


RESULT 2
ABP60419
ID   ABP60419 standard; protein; 281 AA.
XX
AC   ABP60419;
XX
DT   27-MAR-2003  (first entry)
XX
DE   Human uPAR exon 4 deletion variant protein SEQ ID NO 2.
XX
KW   Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW   cancer; receptor.
XX
OS   Homo sapiens.
XX
PN   DE10117381-A1.
XX
PD   10-OCT-2002.
XX
PF   06-APR-2001; 2001DE-01017381.
XX
PR   06-APR-2001; 2001DE-01017381.
XX
PA   (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI   Luther T,  Magdolen V,  Schmitt M,  Muehlenweg B;
XX
DR   WPI; 2003-168688/17.
DR   N-PSDB; ABZ26096.
XX
PT   New nucleic acid encoding a deletion variant of a urokinase receptor
PT   which has one of two exons missing, is useful to detect and treat cancer,
PT   particularly breast and ovarian cancer.
XX
PS   Disclosure; Fig 1; 28pp; German.
XX
CC   The invention relates to a nucleic acid encoding a deletion variant of a
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 4 deletion variant protein of the
CC   invention
XX
SQ   Sequence 281 AA;

  Query Match            97.4%;  Score 1271.5;  DB 6;  Length 281;
  Best Local Similarity   83.6%;  Pred. No. 4.3e-95;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
              |||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPG 120

Qy        104 ----------------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFL 135
                                           :||||||||||||||||||||||||||||||
Db        121 CPGSNGFHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFL 180

Qy        136 IDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCN 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCN 240

Qy        196 HPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
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Db        241 HPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 281


RESULT 3
ABP60421
ID   ABP60421 standard; protein; 290 AA.
XX
AC   ABP60421;
XX
DT   27-MAR-2003  (first entry)
XX
DE   Human uPAR exon 5 deletion variant protein SEQ ID NO 6.
XX
KW   Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW   cancer; receptor.
XX
OS   Homo sapiens.
XX
PN   DE10117381-A1.
XX
PD   10-OCT-2002.
XX
PF   06-APR-2001; 2001DE-01017381.
XX
PR   06-APR-2001; 2001DE-01017381.
XX
PA   (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI   Luther T,  Magdolen V,  Schmitt M,  Muehlenweg B;
XX
DR   WPI; 2003-168688/17.
DR   N-PSDB; ABZ26098.
XX
PT   New nucleic acid encoding a deletion variant of a urokinase receptor
PT   which has one of two exons missing, is useful to detect and treat cancer,
PT   particularly breast and ovarian cancer.
XX
PS   Disclosure; Fig 3; 28pp; German.
XX
CC   The invention relates to a nucleic acid encoding a deletion variant of a
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 5 deletion variant protein of the
CC   invention
XX
SQ   Sequence 290 AA;

  Query Match            97.2%;  Score 1268;  DB 6;  Length 290;
  Best Local Similarity   81.4%;  Pred. No. 8.6e-95;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:58 ; Search time 10.5279 Seconds
(without alignments)
2156.859 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1244.5	95.4	335	2	A39743	u-plasminogen acti
2	782.5	60.0	281	2	S39495	u-plasminogen acti
3	753	57.7	330	1	JN0561	urokinase-type pla
4	704.5	54.0	327	2	A55356	urokinase-type pla
5	684	52.4	328	2	S42152	urinary plasminoge
6	375.5	28.8	222	2	B41643	urokinase-type pla
7	373.5	28.6	222	2	B55356	urokinase-type pla
8	110	8.4	185	1	JC2394	phospholipase A2 i
9	109	8.4	1574	2	T13954	MEGF6 protein - ra
10	106.5	8.2	1046	2	A26838	prestalk protein p
11	101	7.7	18	2	I52614	u-plasminogen acti
12	100	7.7	2139	2	A35672	crumbs protein - f
13	99.5	7.6	601	2	D89711	protein F40E10.4 [
14	99.5	7.6	601	2	T22025	hypothetical prote
15	98.5	7.5	2090	2	T30075	hypothetical prote
16	98.5	7.5	2153	2	T30074	hypothetical prote
17	98	7.5	128	2	I36894	CD59 protein - gre
18	96	7.4	1018	2	T19693	hypothetical prote
19	96	7.4	1463	2	C95032	hypothetical prote
20	96	7.4	2907	2	A57278	fibrillin-2 precur
21	95.5	7.3	1111	2	T26972	hypothetical prote
22	95	7.3	330	2	D96787	protein T4O12.3 [i
23	95	7.3	1463	2	C97903	DNA-directed DNA p
24	94.5	7.2	1558	2	C89114	protein C37C3.6a [
25	94.5	7.2	1790	1	MMFFB1	laminin beta-1 cha
26	94.5	7.2	2167	2	T34395	hypothetical prote
27	94.5	7.2	2871	2	A55567	fibrillin I - bovi
28	94	7.2	126	2	I36914	CD59 protein - bab
29	93.5	7.2	131	2	I56894	complement regulat
30	93	7.1	686	2	JC7569	Delta-4 protein -
31	93	7.1	1820	2	A55494	latent transformin
32	93	7.1	2918	2	A54105	fibrillin-2 precur
33	92.5	7.1	2703	1	A24420	notch protein - fr
34	92	7.0	2871	2	A55624	fibrillin-1 precur
35	91.5	7.0	127	1	A46528	phosphatidylinosit
36	91.5	7.0	130	2	I54553	gene ThB protein -
37	91.5	7.0	1798	2	S53869	laminin beta-2 cha
38	91	7.0	243	2	A33329	testis-specific pr
39	91	7.0	922	2	T23573	hypothetical prote
40	90.5	6.9	1984	2	T13171	probable vitelloge
41	90	6.9	379	2	T16213	APX-1 protein homo
42	89.5	6.9	2813	1	VWHU	von Willebrand fac
43	89	6.8	128	1	RWHU59	surface glycoprote
44	89	6.8	770	2	S04847	leukocyte adhesion
45	89	6.8	771	2	A45839	leukocyte adhesion

ALIGNMENTS

RESULT 1
A39743
u-plasminogen activator receptor form 1 precursor - human
N;Alternate names: monocyte activation antigen Mo3; urokinase-type plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: S12376; A39743; A35242; S34461; I56138; S67529; I39206
R;Roldan, A.L.; Cubellis, M.V.; Masucci, M.T.; Behrendt, N.; Lund, L.R.; Dano, K.; Appel
EMBO J. 9, 467-474, 1990
A;Title: Cloning and expression of the receptor for human urokinase plasminogen activato
A;Reference number: S12376; MUID:90151622; PMID:1689240
A;Accession: S12376
A;Molecule type: mRNA
A;Residues: 1-335 <ROL>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:X51675; NID:g37604; PIDN:CAA35981.1; PID:g
R;Behrendt, N.; Ploug, M.; Patthy, L.; Houen, G.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 7842-7847, 1991
A;Title: The ligand-binding domain of the cell surface receptor for urokinase-type plasm
A;Reference number: A39743; MUID:91210310; PMID:1850423
A;Accession: A39743
A;Molecule type: protein
A;Residues: 23-24,'X',26-27,'XX',30-33,'X',35-38,'X',40,'X',42;110-116,'XX',119,'X' <BEH
A;Cross-references: UNIPARC:UPI00001770BD; UNIPARC:UPI00001770BE
R;Behrendt, N.; Ronne, E.; Ploug, M.; Petri, T.; Lober, D.; Nielsen, L.S.; Schleuning, W
J. Biol. Chem. 265, 6453-6460, 1990
A;Title: The human receptor for urokinase plasminogen activator. NH-2-terminal amino aci
A;Reference number: A35242; MUID:90202929; PMID:2156852
A;Accession: A35242
A;Molecule type: protein
A;Residues: 23,'X',25-38,'H',40-43,'X',45,'X',47-51,'X' <BE2>
A;Cross-references: UNIPARC:UPI0000143F2B
A;Note: the authors show a tentative identification of His for residue 39
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase p
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34461
A;Molecule type: mRNA
A;Residues: 246-335 <PYK>
A;Cross-references: UNIPARC:UPI00001770BF
R;Ploug, M.; Ronne, E.; Behrendt, N.; Jensen, A.L.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 1926-1933, 1991
A;Title: Cellular receptor for urokinase plasminogen activator. Carboxyl-terminal proces
A;Reference number: A38677; MUID:91107700; PMID:1846368
A;Contents: annotation
R;Min, H.Y.; Semnani, R.; Mizukami; I.F.; Watt, K.; Todd, R.F.
J. Immunol. 148, 3636-3642, 1992
A;Title: cDNA for Mo3, a monocyte activation antigen, encodes the human receptor for uro
A;Reference number: I56138; MUID:92268511; PMID:1316922
A;Accession: I56138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

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A;Residues: 1-335 <RES>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:M83246; NID:g188623; PIDN:AAA59862.1; PID:
R;Wang, Y.; Dang, J.; Johnson, L.K.; Selhamer, J.J.; Doe, W.F.
Eur. J. Biochem. 227, 116-122, 1995
A;Title: Structure of the human urokinase receptor gene and its similarity to CD59 and t
A;Reference number: S67529; MUID:95154279; PMID:7531640
A;Accession: S67529
A;Molecule type: DNA
A;Residues: 1-335 <WAN>
A;Cross-references: UNIPARC:UPI000000D8C1
A;Note: the authors translated the codon CGC for residue 51 as Ala
R;Casey, J.R.; Petranka, J.G.; Kottra, J.; Fleenor, D.E.; Rosse, W.F.
Blood 84, 1151-1156, 1994
A;Title: The structure of the urokinase-type plasminogen activator receptor gene.
A;Reference number: I39206; MUID:94325556; PMID:8049431
A;Accession: I39206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <RE2>
A;Cross-references: UNIPARC:UPI000000D8C1; EMBL:U09937; NID:g533374; PIDN:AAB60690.1; PI
C;Genetics:
A;Gene: uPAR
A;Introns: 19/1; 56/1; 104/1; 158/1; 203/1; 252/1
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; glycoprotein; membrane protein; phosphatidylinositol l
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-304/Product: (or 23-305 or 23-306) u-plasminogen activator receptor #status experim
F;23-107/Domain: Ly-6 homology <LY6A>
F;115-206/Domain: Ly-6 homology <LY6B>
F;214-301/Domain: Ly-6 homology <LY6C>
F;74,184,194,222,255/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             95.4%;  Score 1244.5;  DB 2;  Length 335;
  Best Local Similarity   70.1%;  Pred. No. 5.8e-91;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   99;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :|||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              |||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 2
S39495
u-plasminogen activator receptor form 2 precursor - human
N;Alternate names: urokinase-type plasminogen activator receptor form 2
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S39495; S34462
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
submitted to the EMBL Data Library, December 1993
A;Description: An alternatively spliced variant of mRNA for the human receptor for uroki
A;Reference number: S39495
A;Accession: S39495
A;Molecule type: mRNA
A;Residues: 1-281 <PYK1>
A;Cross-references: UNIPROT:Q03405; UNIPARC:UPI000002B696; EMBL:X74039; NID:g456192; PID
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase p
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34462
A;Molecule type: mRNA
A;Residues: 246-281 <PYK2>
A;Cross-references: UNIPARC:UPI000016A0A4; GB:U09347; GB:S63673; NID:g483827; PIDN:AAA17
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; receptor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-281/Product: u-plasminogen activator receptor #status predicted <MAT>
F;115-206/Domain: Ly-6 homology <LY6>

  Query Match             60.0%;  Score 782.5;  DB 2;  Length 281;
  Best Local Similarity   60.3%;  Pred. No. 1.4e-54;
  Matches  152;  Conservative    1;  Mismatches    0;  Indels   99;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :|||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHE 153
              ||||||||||||
Db        241 MNQCLVATGTHE 252


RESULT 3
JN0561
urokinase-type plasminogen activator receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: JN0561; I46977
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and induc
A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0561
A;Molecule type: mRNA
A;Residues: 1-330 <KRA>
A;Cross-references: UNIPROT:Q05588; UNIPARC:UPI0000137CC6; GB:L03545; NID:g163802; PIDN:
R;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U.
Thromb. Res. 72, 59-70, 1993
A;Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen activator r
A;Reference number: I46977; MUID:94167671; PMID:8122188
A;Accession: I46977
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <REU>
A;Cross-references: UNIPARC:UPI0000137CC6; GB:S70635; NID:g545770; PIDN:AAB30120.1; PID
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-300/Product: urokinase-type plasminogen activator receptor #status predicted <MAT>
F;21-104/Domain: Ly-6 homology <LY6A>
F;113-201/Domain: Ly-6 homology <LY6B>
F;209-296/Domain: Ly-6 homology <LY6C>
F;301-330/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:28 ; Search time 56.7336 Seconds
(without alignments)
2934.852 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1244.5	95.4	335	1	UPAR_HUMAN	Q03405 homo sapien
2	1242.5	95.2	335	1	UPAR_PANTR	Q9gk80 pan troglod
3	1184.5	90.8	335	1	UPAR_CERAE	Q9gk79 cercopithec
4	1184.5	90.8	335	1	UPAR_MACFA	Q9gk78 macaca fasc
5	1061.5	81.3	301	2	Q9BWT0_HUMAN	Q9bwt0 homo sapien
6	975	74.7	336	2	Q9GK77_AOTTR	Q9gk77 aotus trivi
7	782.5	60.0	281	2	Q6IB52_HUMAN	Q6ib52 homo sapien
8	777.5	59.6	251	2	Q9UPI5_HUMAN	Q9upi5 homo sapien
9	753	57.7	330	1	UPAR_BOVIN	Q05588 bos taurus
10	713	54.6	328	2	O35771_RAT	O35771 rattus norv
11	704.5	54.0	327	1	UPAR_MOUSE	P35456 mus musculu
12	704.5	54.0	327	2	Q545X5_MOUSE	Q545x5 mus musculu
13	704	53.9	322	2	Q9R119_CRIGR	Q9r119 cricetulus
14	650	49.8	328	1	UPAR_RAT	P49616 rattus norv
15	375.5	28.8	222	1	UPAS_MOUSE	P35457 mus musculu
16	373.5	28.6	222	2	Q91Z14_MOUSE	Q91z14 mus musculu
17	359	27.5	220	1	UPAS_RAT	P51573 rattus norv
18	322	24.7	204	2	Q9TVA9_BOVIN	Q9tva9 bos taurus
19	256.5	19.7	88	2	Q9N124_HORSE	Q9n124 equus cabal
20	167	12.8	199	2	Q4FAD9_9SALA	Q4fad9 desmognathu
21	166.5	12.8	217	2	Q566G7_XENLA	Q566g7 xenopus lae
22	164	12.6	199	2	Q4FAD7_9SALA	Q4fad7 desmognathu
23	164	12.6	205	2	Q4FAG4_9SALA	Q4fag4 plethodon m
24	163	12.5	199	2	Q4FAD6_9SALA	Q4fad6 desmognathu
25	163	12.5	205	2	Q4FAH3_9SALA	Q4fah3 plethodon m
26	160	12.3	39	2	Q4RCT4_TETNG	Q4rct4 tetraodon n
27	160	12.3	196	2	Q4FAD0_9SALA	Q4fad0 aneides fer
28	160	12.3	205	2	Q4FAH1_9SALA	Q4fah1 plethodon m
29	159	12.2	199	2	Q4FAD3_9SALA	Q4fad3 desmognathu
30	158	12.1	199	2	Q4FAG8_9SALA	Q4fag8 plethodon m
31	158	12.1	205	2	Q4FAG7_PLEJO	Q4fag7 plethodon j
32	158	12.1	205	2	Q4FAG5_9SALA	Q4fag5 plethodon s
33	158	12.1	205	2	Q4FAG6_9SALA	Q4fag6 plethodon c
34	157	12.0	199	2	Q4FAE1_9SALA	Q4fae1 plethodon s
35	157	12.0	205	2	Q4FAH4_9SALA	Q4fah4 plethodon t
36	155	11.9	196	2	Q4FAD1_9SALA	Q4fad1 aneides fer
37	155	11.9	199	2	Q4FAE0_9SALA	Q4fae0 desmognathu
38	153	11.7	199	2	Q4FAG2_9SALA	Q4fag2 plethodon t
39	151	11.6	199	2	Q4FAH8_9SALA	Q4fah8 plethodon w
40	151	11.6	199	2	Q4FAG9_9SALA	Q4fag9 plethodon w
41	150	11.5	199	2	Q4FAH5_9SALA	Q4fah5 plethodon w
42	150	11.5	205	2	Q4FAG0_PLEJO	Q4fag0 plethodon j
43	150	11.5	205	2	Q4FAF6_9SALA	Q4faf6 plethodon c
44	148	11.3	199	2	Q4FAH2_9SALA	Q4fah2 plethodon w
45	148	11.3	212	2	Q9CQD7_MOUSE	Q9cqd7 m mus muscu

ALIGNMENTS

RESULT 1
UPAR_HUMAN
ID UPAR_HUMAN STANDARD; PRT; 335 AA.
AC Q03405; Q12876; Q15845; Q16887; Q9NYC8; Q9UD69; Q9UEA6; Q9UM92;
AC Q9UMV0;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE PAR) (Monocyte activation antigen Mo3) (CD87 antigen).
GN Name=PLAUR; Synonyms=MO3, UPAR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-33.
RX MEDLINE=90151622; PubMed=1689240;
RA Roldan A.L., Cubellis M.V., Masucci M.T., Behrendt N., Lund L.R.,
RA Danoe K., Appella E., Blasi F.;
RT "Cloning and expression of the receptor for human urokinase
RT plasminogen activator, a central molecule in cell surface, plasmin
RT dependent proteolysis.";
RL EMBO J. 9:467-474(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=92268511; PubMed=1316922;
RA Min H.Y., Semnani R., Mizukami I.F., Watt K., Todd R.F. III, Liu D.Y.;
RT "cDNA for Mo3, a monocyte activation antigen, encodes the human
RT receptor for urokinase plasminogen activator.";
RL J. Immunol. 148:3636-3642(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RX MEDLINE=94178507; PubMed=8131971;
RA Bayraktutan U., Jones P.;
RT "A novel urokinase receptor on monocyte-like macrophage cell line.";
RL Biochem. Soc. Trans. 21:395-395(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX MEDLINE=93314820; PubMed=8392005; DOI=10.1016/0014-5793(93)81763-P;
RA Pyke C., Eriksen J., Solberg H., Schnack Nielsen B., Kristensen P.,
RA Lund L.R., Danoe K.;
RT "An alternatively spliced variant of mRNA for the human receptor for
RT urokinase plasminogen activator.";
RL FEBS Lett. 326:69-74(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 3).
RC TISSUE=Placenta;
RX MEDLINE=94325556; PubMed=8049431;
RA Casey J.R., Petranka J.G., Kottra J., Fleenor D.E., Rosse W.F.;
RT "The structure of the urokinase-type plasminogen activator receptor
RT gene.";
RL Blood 84:1151-1156(1994).

RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLY-55; ALA-86;
RP GLN-105; ARG-220; LYS-281 AND PRO-317.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP NUCLEOTIDE SEQUENCE OF 1-322 (ISOFORM 1).
RC TISSUE=Lung cancer;
RA Zhu F., Jia S., He F.;
RT "Molecular cloning of UPAR from a human giant cell lung cancer cell
RT line.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE OF 1-18.
RX MEDLINE=95329719; PubMed=7605992;
RA Soravia E., Grebe A., De Luca P., Helin K., Suh T.T., Degen J.L.,
RA Blasi F.;
RT "A conserved TATA-less proximal promoter drives basal transcription
RT from the urokinase-type plasminogen activator receptor gene.";
RL Blood 86:624-635(1995).
RN [11]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=90202929; PubMed=2156852;
RA Behrendt N., Roenne E., Ploug M., Petri T., Loeber D., Nielsen L.S.,
RA Schleuning W.-D., Blasi F., Appella E., Danoe K.;
RT "The human receptor for urokinase plasminogen activator. NH2-terminal
RT amino acid sequence and glycosylation variants.";
RL J. Biol. Chem. 265:6453-6460(1990).
RN [12]
RP PROTEIN SEQUENCE OF 106-116, AND CLEAVAGE BY U-PA.
RX MEDLINE=97182578; PubMed=9030717;
RA Hoeyer-Hansen G., Ploug M., Behrendt N., Roenne E., Danoe K.;
RT "Cell-surface acceleration of urokinase-catalyzed receptor cleavage.";
RL Eur. J. Biochem. 243:21-26(1997).
RN [13]
RP DISULFIDE BONDS, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=93352546; PubMed=8394346;
RA Ploug M., Kjalke M., Roenne E., Weidle U., Hoeyer-Hansen G., Danoe K.;
RT "Localization of the disulfide bonds in the NH2-terminal domain of the
RT cellular receptor for human urokinase-type plasminogen activator. A
RT domain structure belonging to a novel superfamily of glycolipid-
RT anchored membrane proteins.";
RL J. Biol. Chem. 268:17539-17546(1993).
CC -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC Plays a role in localizing and promoting plasmin formation.
CC Mediates the proteolysis-independent signal transduction
CC activation effects of U-PA. It is subject to negative-feedback
CC regulation by U-PA which cleaves it into an inactive form.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (isoform 1). Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=uPAR1, GPI-anchored;
CC IsoId=Q03405-1; Sequence=Displayed;
CC Name=2; Synonyms=uPAR2, Secreted;
CC IsoId=Q03405-2; Sequence=VSP_006715;
CC Name=3;
CC IsoId=Q03405-3; Sequence=VSP_006714;
CC -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR EMBL; X51675; CAA35981.1; -; mRNA.
DR EMBL; M83246; AAA59862.1; -; mRNA.
DR EMBL; X74039; CAA52191.1; -; mRNA.
DR EMBL; U09346; AAA17979.1; -; Unassigned_DNA.
DR EMBL; U09347; AAA17978.1; -; mRNA.
DR EMBL; U09937; AAB60690.1; -; Genomic_DNA.
DR EMBL; U09931; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09932; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09933; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09935; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09936; AAB60690.1; JOINED; Genomic_DNA.
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DR EMBL; AY194849; AAN86351.1; -; Genomic_DNA.
DR EMBL; AC005525; AAC32739.1; -; Genomic_DNA.
DR EMBL; AC006953; AAD17388.1; -; Genomic_DNA.
DR EMBL; AC006953; AAD17387.1; -; Genomic_DNA.
DR EMBL; BC002788; AAH02788.1; -; mRNA.
DR EMBL; AF257789; AAF71751.1; -; mRNA.
DR EMBL; S78532; AAD14289.1; -; Genomic_DNA.
DR EMBL; A18757; CAA01421.1; -; Unassigned_RNA.
DR PIR; I52614; I52614.
DR PIR; S39495; S39495.
DR Ensembl; ENSG00000011422; Homo sapiens.
DR HGNC; HGNC:9053; PLAUR.
DR H-InvDB; HIX0015192; -.
DR Reactome; Q03405; -.
DR MIM; 173391; -.
DR GO; GO:0009986; C:cell surface; IEP.
DR GO; GO:0019898; C:extrinsic to membrane; TAS.

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DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.

  Query Match             95.4%;  Score 1244.5;  DB 1;  Length 335;
  Best Local Similarity   70.1%;  Pred. No. 1.1e-99;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   99;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              ||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 2
UPAR_PANTR
ID   UPAR_PANTR     STANDARD;      PRT;   335 AA.
AC   Q9GK80;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE   PAR).
GN   Name=PLAUR; Synonyms=UPAR;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Skin;
RX   MEDLINE=21245115; PubMed=11347891; DOI=10.1515/BC.2001.053;
RA   Engelholm L.H., Behrendt N.;
RT   "Differential binding of urokinase and peptide antagonists to the
RT   urokinase receptor: evidence from characterization of the receptor in
RT   four primate species.";
RL   Biol. Chem. 382:435-442(2001).
CC   -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC       Plays a role in localizing and promoting plasmin formation.
CC       Mediates the proteolysis-independent signal transduction
CC       activation effects of U-PA. It is subject to negative-feedback
CC       regulation by U-PA which cleaves it into an inactive form (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF302071; AAG40759.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   InterPro; IPR003631; U-PAR_recept.
DR   Pfam; PF00021; UPAR_LY6; 2.
DR   ProDom; PD007582; U-PAR_recept; 1.
DR   PROSITE; PS00983; LY6_UPAR; 3.
KW   Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Repeat;
KW   Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23   ?305       Urokinase plasminogen activator surface
FT                                receptor.
FT   PROPEP    ?306    335       Removed in mature form (Potential).
FT   DOMAIN      23    114       UPAR/Ly6 1.
FT   DOMAIN     115    213       UPAR/Ly6 2.
FT   DOMAIN     214    305       UPAR/Ly6 3.
FT   SITE       105    106       Cleavage (by U-PA) (By similarity).
FT   SITE       111    112       Cleavage (by U-PA) (By similarity).
FT   LIPID      305    305       GPI-anchor amidated glycine (Potential).
FT   CARBOHYD    74     74       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   124    124       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   184    184       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   194    194       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   222    222       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   255    255       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    25     46       By similarity.
FT   DISULFID    28     34       By similarity.
FT   DISULFID    39     67       By similarity.
FT   DISULFID    93     98       By similarity.
FT   DISULFID   117    144       Potential.
FT   DISULFID   120    127       Potential.
FT   DISULFID   137    169       Potential.
FT   DISULFID   175    192       Potential.
FT   DISULFID   193    198       Potential.
FT   DISULFID   216    244       Potential.
FT   DISULFID   219    227       Potential.
FT   DISULFID   237    263       Potential.
FT   DISULFID   269    287       Potential.
FT   DISULFID   288    293       Potential.
SQ   SEQUENCE   335 AA;  37022 MW;  C56F3A1621BA2D64 CRC64;

  Query Match             95.2%;  Score 1242.5;  DB 1;  Length 335;
  Best Local Similarity   69.9%;  Pred. No. 1.7e-99;
  Matches  234;  Conservative    2;  Mismatches    0;  Indels   99;  Gaps    1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRMWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSNMSCERGRHQSLQCRNPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              ||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 3
UPAR_CERAE
ID   UPAR_CERAE     STANDARD;      PRT;   335 AA.
AC   Q9GK79;
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DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE   PAR).
GN   Name=PLAUR; Synonyms=UPAR;
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21245115; PubMed=11347891; DOI=10.1515/BC.2001.053;
RA   Engelholm L.H., Behrendt N.;
RT   "Differential binding of urokinase and peptide antagonists to the
RT   urokinase receptor: evidence from characterization of the receptor in
RT   four primate species.";
RL   Biol. Chem. 382:435-442(2001).
CC   -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC       Plays a role in localizing and promoting plasmin formation.
CC       Mediates the proteolysis-independent signal transduction
CC       activation effects of U-PA. It is subject to negative-feedback
CC       regulation by U-PA which cleaves it into an inactive form (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF302072; AAG40760.1; -; mRNA.
DR   InterPro; IPR001526; LY6_UPAR.
DR   InterPro; IPR003631; U-PAR_recept.
DR   Pfam; PF00021; UPAR_LY6; 2.
DR   ProDom; PD007582; U-PAR_recept; 1.
DR   SMART; SM00134; LU; 3.
DR   PROSITE; PS00983; LY6_UPAR; 3.
KW   Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Repeat;
KW   Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23   ?305       Urokinase plasminogen activator surface
FT                                receptor.
FT   PROPEP     ?306    335       Removed in mature form (Potential).
FT   DOMAIN       23    114       UPAR/Ly6 1.
FT   DOMAIN      115    213       UPAR/Ly6 2.
FT   DOMAIN      214    305       UPAR/Ly6 3.
FT   SITE        105    106       Cleavage (by U-PA) (By similarity).
FT   SITE        111    112       Cleavage (by U-PA) (By similarity).
FT   LIPID       305    305       GPI-anchor amidated glycine (Potential).
FT   CARBOHYD     74     74       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    184    184       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    194    194       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    255    255       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     25     46       By similarity.
FT   DISULFID     28     34       By similarity.
FT   DISULFID     39     67       By similarity.
FT   DISULFID     93     98       By similarity.
FT   DISULFID    117    144       Potential.
FT   DISULFID    120    127       Potential.
FT   DISULFID    137    169       Potential.
FT   DISULFID    175    192       Potential.
FT   DISULFID    193    198       Potential.
FT   DISULFID    216    244       Potential.
FT   DISULFID    219    227       Potential.
FT   DISULFID    237    263       Potential.
FT   DISULFID    269    287       Potential.
FT   DISULFID    288    293       Potential.
SQ   SEQUENCE   335 AA;  37187 MW;  9974EA89D1F47CEC CRC64;

  Query Match             90.8%;  Score 1184.5;  DB 1;  Length 335;
  Best Local Similarity   66.6%;  Pred. No. 1.8e-94;
  Matches  223;  Conservative    7;  Mismatches    6;  Indels   99;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              |||| |||||||||||||||||||||||:|||||||||||||||||||||:|||||||
Db          1 MGHPLLLPLLLLLHTCVPASWGLRCMQCKSNGDCRVEECALGQDLCRTTIVRMWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||:|||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTMSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTFSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDMVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :|||||||||| |||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGHQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              |||||||||:|||||||||||| |||||| |||||||||||:| |||:||||||||||
Db        241 MNQCLVATGTYEPKNQSYMVRGCVTASMCQRAHLGDAFSMNHINVFCCTESGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              ||| |||||||||||||||||||||||||||||||
Db        301 QYRKGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 4
UPAR_MACFA
ID   UPAR_MACFA     STANDARD;      PRT;   335 AA.
AC   Q9GK78;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE   PAR).
GN   Name=PLAUR; Synonyms=UPAR;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21245115; PubMed=11347891; DOI=10.1515/BC.2001.053;
RA   Engelholm L.H., Behrendt N.;
RT   "Differential binding of urokinase and peptide antagonists to the
RT   urokinase receptor: evidence from characterization of the receptor in
RT   four primate species.";
RL   Biol. Chem. 382:435-442(2001).
CC   -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC       Plays a role in localizing and promoting plasmin formation.
CC       Mediates the proteolysis-independent signal transduction
CC       activation effects of U-PA. It is subject to negative-feedback
CC       regulation by U-PA which cleaves it into an inactive form (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF302073; AAG40761.1; -; mRNA.
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:13 ; Search time 17.254 Seconds
(without alignments)
1130.835 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1244.5	95.4	335	1	US-08-085-122-13	Sequence 13, Appl
2	1244.5	95.4	335	2	US-08-442-108B-23	Sequence 23, Appl
3	1244.5	95.4	335	2	US-09-949-002-346	Sequence 346, App
4	1244.5	95.4	417	2	US-09-949-002-527	Sequence 527, App
5	515	39.5	90	1	US-08-085-122-5	Sequence 5, Appli
6	515	39.5	90	1	US-08-319-052-5	Sequence 5, Appli
7	515	39.5	90	2	US-08-442-108B-5	Sequence 5, Appli
8	437	33.5	92	1	US-08-085-122-3	Sequence 3, Appli
9	437	33.5	92	1	US-08-319-052-3	Sequence 3, Appli
10	437	33.5	92	2	US-08-442-108B-3	Sequence 3, Appli
11	183	14.0	34	1	US-08-085-122-11	Sequence 11, Appl
12	183	14.0	34	1	US-08-319-052-21	Sequence 21, Appl
13	183	14.0	34	2	US-08-442-108B-21	Sequence 21, Appl
14	158.5	12.1	204	1	US-08-652-859-2	Sequence 2, Appli
15	158.5	12.1	204	1	US-08-919-706-2	Sequence 2, Appli
16	158.5	12.1	204	1	US-09-153-751-2	Sequence 2, Appli
17	158.5	12.1	204	2	US-09-886-319A-38	Sequence 38, Appl
18	158.5	12.1	228	2	US-09-886-319A-45	Sequence 45, Appl
19	148	11.3	212	2	US-09-886-319A-37	Sequence 37, Appl
20	146	11.2	346	2	US-09-991-181-197	Sequence 197, App
21	146	11.2	346	2	US-09-990-444-197	Sequence 197, App
22	146	11.2	346	2	US-09-997-333-197	Sequence 197, App
23	146	11.2	346	2	US-09-992-598-197	Sequence 197, App
24	133	10.2	220	2	US-09-844-497-2	Sequence 2, Appli
25	133	10.2	220	2	US-10-404-170-2	Sequence 2, Appli
26	127	9.7	30	1	US-08-085-122-2	Sequence 2, Appli
27	127	9.7	30	1	US-08-319-052-2	Sequence 2, Appli
28	127	9.7	30	2	US-08-442-108B-2	Sequence 2, Appli
29	126.5	9.7	273	2	US-09-270-767-41968	Sequence 41968, A
30	120	9.2	197	2	US-09-886-319A-81	Sequence 81, Appl
31	117	9.0	21	2	US-08-657-339A-11	Sequence 11, Appl
32	117	9.0	21	2	US-08-457-694A-11	Sequence 11, Appl
33	116	8.9	116	2	US-09-621-976-7212	Sequence 7212, Ap
34	107.5	8.2	89	2	US-09-513-999C-7333	Sequence 7333, Ap
35	103.5	7.9	350	2	US-09-134-618-6	Sequence 6, Appli
36	103.5	7.9	440	2	US-08-883-036A-2	Sequence 2, Appli
37	103.5	7.9	440	2	US-09-536-201-2	Sequence 2, Appli
38	103.5	7.9	440	2	US-09-578-392-2	Sequence 2, Appli
39	100.5	7.7	141	2	US-09-825-294-215	Sequence 215, App
40	100.5	7.7	141	2	US-09-970-966-215	Sequence 215, App
41	99.5	7.6	735	2	US-09-191-647-9	Sequence 9, Appli
42	99.5	7.6	735	2	US-09-540-245A-9	Sequence 9, Appli
43	99.5	7.6	735	2	US-09-540-153-9	Sequence 9, Appli
44	99.5	7.6	735	2	US-10-289-776-9	Sequence 9, Appli
45	98	7.5	775	2	US-09-786-256C-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-085-122-13
; Sequence 13, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-085-122-13

Query Match 95.4%; Score 1244.5; DB 1; Length 335;
Best Local Similarity 70.1%; Pred. No. 4.1e-115;
Matches 235; Conservative 1; Mismatches 0; Indels 99; Gaps 1;

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Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
              |||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335
```

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RESULT 2
US-08-442-108B-23
; Sequence 23, Application US/08442108B
; Patent No. 6248712
;  GENERAL INFORMATION:
;    APPLICANT:  DANO, KELD
;    APPLICANT:  BLASI, FRANCESCO
;    APPLICANT:  ROLDAN, ANN LOURING
;    APPLICANT:  CUBELLIS, MARIA VITTORIA
;    APPLICANT:  MASUCCI, MARIA TERESA
;    APPLICANT:  APPELLA, ETTORE
;    APPLICANT:  SCHLEUNING, WOLF-DIETER
;    APPLICANT:  BEHRENDT, NIELS
;    APPLICANT:  KRISTENSEN, PETER
;    APPLICANT:  POLLANEN, JARI
;    APPLICANT:  SALONEN, EEVA-MARJATTA
;    TITLE OF INVENTION:  UROKINASE-TYPE PLASMINOGEN ACTIVATOR
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,108B
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/319,052
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/824,189
;      FILING DATE:  06-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/DK90/00090
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/374,854
;      FILING DATE:  03-JUL-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/334,613
;      FILING DATE:  07-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  DANO=1D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-442-108B-23

  Query Match             95.4%;  Score 1244.5;  DB 2;  Length 335;
  Best Local Similarity   70.1%;  Pred. No. 4.1e-115;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   99;  Gaps    1;

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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS----------------- 103
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Qy        104 ------------------------------------------------------------ 103

Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        104 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 141
                                     :||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        142 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        202 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
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Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 3
US-09-949-002-346
; Sequence 346, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-346

  Query Match             95.4%;  Score 1244.5;  DB 2;  Length 335;
  Best Local Similarity   70.1%;  Pred. No. 4.1e-115;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   99;  Gaps    1;
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:34 ; Search time 49.1301 Seconds
(without alignments)
2007.073 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1305	100.0	236	4	US-10-679-951-4	Sequence 4, Appli
2	1290.5	98.9	235	4	US-10-679-951-10	Sequence 10, Appl
3	1271.5	97.4	281	4	US-10-679-951-2	Sequence 2, Appli
4	1271.5	97.4	281	4	US-10-679-951-9	Sequence 9, Appli
5	1268	97.2	290	4	US-10-679-951-6	Sequence 6, Appli
6	1262.5	96.7	289	4	US-10-679-951-11	Sequence 11, Appl
7	1244.5	95.4	335	4	US-10-193-656-6	Sequence 6, Appli
8	1244.5	95.4	335	4	US-10-177-293-362	Sequence 362, App
9	1244.5	95.4	335	4	US-10-295-027-1327	Sequence 1327, Ap
10	1244.5	95.4	335	4	US-10-429-160-75	Sequence 75, Appl
11	1244.5	95.4	335	4	US-10-679-951-8	Sequence 8, Appli
12	1244.5	95.4	335	5	US-10-783-528-97	Sequence 97, Appl
13	1244.5	95.4	335	5	US-10-723-860-2344	Sequence 2344, Ap
14	1244.5	95.4	335	5	US-10-482-029-160	Sequence 160, App
15	1237.5	94.8	287	4	US-10-087-192-1806	Sequence 1806, Ap
16	1061.5	81.3	301	4	US-10-755-889-424	Sequence 424, App
17	957.5	73.4	283	5	US-10-993-007-1	Sequence 1, Appli
18	704.5	54.0	327	4	US-10-087-192-1803	Sequence 1803, Ap
19	515	39.5	90	3	US-09-755-109-5	Sequence 5, Appli
20	437	33.5	92	3	US-09-755-109-3	Sequence 3, Appli
21	183	14.0	34	3	US-09-755-109-21	Sequence 21, Appl
22	158.5	12.1	204	3	US-09-886-319A-38	Sequence 38, Appl
23	158.5	12.1	204	3	US-09-875-520-2	Sequence 2, Appli
24	158.5	12.1	204	4	US-10-376-564-38	Sequence 38, Appl
25	158.5	12.1	228	3	US-09-886-319A-45	Sequence 45, Appl
26	158.5	12.1	228	4	US-10-376-564-45	Sequence 45, Appl
27	153	11.7	366	5	US-10-450-763-45496	Sequence 45496, A
28	148	11.3	212	3	US-09-886-319A-37	Sequence 37, Appl
29	148	11.3	212	4	US-10-376-564-37	Sequence 37, Appl
30	146	11.2	346	3	US-09-989-722-197	Sequence 197, App
31	146	11.2	346	3	US-09-989-723-197	Sequence 197, App
32	146	11.2	346	3	US-09-989-279-197	Sequence 197, App
33	146	11.2	346	3	US-09-989-727-197	Sequence 197, App
34	146	11.2	346	3	US-09-989-731-197	Sequence 197, App
35	146	11.2	346	3	US-09-989-732-197	Sequence 197, App
36	146	11.2	346	3	US-09-991-073-197	Sequence 197, App
37	146	11.2	346	3	US-09-990-442-197	Sequence 197, App
38	146	11.2	346	3	US-09-991-163-197	Sequence 197, App
39	146	11.2	346	3	US-09-993-604-197	Sequence 197, App
40	146	11.2	346	3	US-09-990-456-197	Sequence 197, App
41	146	11.2	346	3	US-09-989-721-197	Sequence 197, App
42	146	11.2	346	3	US-09-992-598-197	Sequence 197, App
43	146	11.2	346	3	US-09-989-293A-197	Sequence 197, App
44	146	11.2	346	3	US-09-989-735-197	Sequence 197, App
45	146	11.2	346	3	US-09-990-444-197	Sequence 197, App

ALIGNMENTS

RESULT 1
US-10-679-951-4
; Sequence 4, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnostic
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-679-951-4

Query Match 100.0%; Score 1305; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 8.7e-112;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSVLELENLPQNGRQCYSC 120
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Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSVLELENLPQNGRQCYSC 120

Qy        121 KGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFS 180
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Db        121 KGNSTHGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFS 180

Qy        181 MNHIDVSCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
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Db        181 MNHIDVSCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 236
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RESULT 2

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US-10-679-951-10
; Sequence 10, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-679-951-10

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  Matches  235;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
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RESULT 3
US-10-679-951-2
; Sequence 2, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-679-951-2

  Query Match             97.4%;  Score 1271.5;  DB 4;  Length 281;
  Best Local Similarity   83.6%;  Pred. No. 1.3e-108;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
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Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRPKDDRHLRGCGYLPG 120

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; Sequence 9, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-679-951-9

  Query Match             97.4%;  Score 1271.5;  DB 4;  Length 281;
  Best Local Similarity   83.6%;  Pred. No. 1.3e-108;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNS---------------- 103
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Qy        104 ---------------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFL 135
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Qy        136 IDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCN 195
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Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:54:24 ; Search time 4.38662 Seconds
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545.203 Million cell updates/sec

Title: US-10-679-951-4
Perfect score: 1305
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	146	11.2	346	6	US-10-131-826A-432	Sequence 432, App
2	146	11.2	346	6	US-10-967-457-77	Sequence 77, Appl
3	116	8.9	1418	6	US-10-453-372-864	Sequence 864, App
4	109	8.4	1574	6	US-10-055-877-211	Sequence 211, App
5	105	8.0	1198	6	US-10-453-372-880	Sequence 880, App
6	105	8.0	1398	6	US-10-055-877-46	Sequence 46, Appl
7	105	8.0	1398	6	US-10-453-372-872	Sequence 872, App
8	105	8.0	1450	6	US-10-055-877-48	Sequence 48, Appl
9	105	8.0	1450	6	US-10-453-372-874	Sequence 874, App
10	105	8.0	1594	6	US-10-453-372-860	Sequence 860, App
11	104	8.0	1403	6	US-10-055-877-52	Sequence 52, Appl
12	104	8.0	1403	6	US-10-453-372-878	Sequence 878, App
13	104	8.0	1404	6	US-10-055-877-44	Sequence 44, Appl
14	104	8.0	1404	6	US-10-453-372-870	Sequence 870, App
15	104	8.0	1547	6	US-10-453-372-886	Sequence 886, App
16	104	8.0	1577	6	US-10-055-877-54	Sequence 54, Appl
17	104	8.0	1577	6	US-10-453-372-882	Sequence 882, App
18	104	8.0	1577	6	US-10-453-372-884	Sequence 884, App
19	104	8.0	1620	6	US-10-453-372-868	Sequence 868, App
20	104	8.0	1653	6	US-10-453-372-866	Sequence 866, App
21	97.5	7.5	1140	6	US-10-055-877-215	Sequence 215, App
22	94.5	7.2	126	7	US-11-116-939-4	Sequence 4, Appli
23	92	7.0	533	7	US-11-128-059-58	Sequence 58, Appl
24	92	7.0	1416	7	US-11-128-059-60	Sequence 60, Appl
25	92	7.0	1494	7	US-11-128-059-78	Sequence 78, Appl
26	92	7.0	2086	7	US-11-128-059-82	Sequence 82, Appl
27	92	7.0	2313	7	US-11-128-059-80	Sequence 80, Appl
28	92	7.0	2358	7	US-11-128-059-74	Sequence 74, Appl
29	92	7.0	2439	7	US-11-128-059-76	Sequence 76, Appl
30	92	7.0	2458	7	US-11-128-059-94	Sequence 94, Appl
31	92	7.0	2551	6	US-10-453-372-256	Sequence 256, App
32	92	7.0	2551	7	US-11-128-059-96	Sequence 96, Appl
33	91.5	7.0	1798	6	US-10-995-561-1033	Sequence 1033, Ap
34	91.5	7.0	1798	6	US-10-995-561-1034	Sequence 1034, Ap
35	91	7.0	969	6	US-10-055-877-214	Sequence 214, App
36	90.5	6.9	997	7	US-11-113-424-37	Sequence 37, Appl
37	89.5	6.9	2764	6	US-10-995-561-691	Sequence 691, App
38	89.5	6.9	2813	6	US-10-995-561-688	Sequence 688, App
39	89.5	6.9	2919	6	US-10-821-234-1133	Sequence 1133, Ap
40	89	6.8	128	6	US-10-821-234-1538	Sequence 1538, Ap
41	89	6.8	419	7	US-11-113-202-4	Sequence 4, Appli
42	88.5	6.8	703	6	US-10-821-234-1412	Sequence 1412, Ap
43	88.5	6.8	1400	6	US-10-821-234-1045	Sequence 1045, Ap
44	88	6.7	419	7	US-11-113-202-23	Sequence 23, Appl
45	88	6.7	999	7	US-11-113-424-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-131-826A-432
; Sequence 432, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.

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;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 432
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-432

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  Matches   64;  Conservative   22;  Mismatches  119;  Indels   44;  Gaps   12;

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              |||||      |   | |  |  | :  |      :  :|| | |:|   :  :     :
Db         20 LLLLLRGGAQA---LECYSCVQKADDGCSPNKMKTVKCAPGVDVCTEAVGAVETIHGQFS 76

Qy         62 LVEKSCTHS--EKTNRTLSYRTGLKITSLTEVVCGLDLCN------------QGNSVLEL 107
              |  : |       | :| |      |     | :  |  | ||               ||
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Qy        162 RGCATASMC-QHAHLGDAFSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHL 216
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Qy        217 SLTITLLMT 225
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RESULT 2
US-10-967-457-77
; Sequence 77, Application US/10967457
; Publication No. US20050244931A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF545PCT
;  CURRENT APPLICATION NUMBER: US/10/967,457
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: US/09/833,041
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/229,358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256,931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199,384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-967-457-77

  Query Match             11.2%;  Score 146;  DB 6;  Length 346;
  Best Local Similarity   25.7%;  Pred. No. 1e-06;
  Matches   64;  Conservative   22;  Mismatches  119;  Indels   44;  Gaps   12;

Qy          9 LLLLLHTCVPASWGLRCMQC--KTNGDC-----RVEECALGQDLCRTTIVRLWEEGEELE 61
              |||||      |   | |  |  | :  |      :  :|| | |:|   :  :     :
Db         20 LLLLLRGGAQA---LECYSCVQKADDGCSPNKMKTVKCAPGVDVCTEAVGAVETIHGQFS 76

Qy         62 LVEKSCTHS--EKTNRTLSYRTGLKITSLTEVVCGLDLCN------------QGNSVLEL 107
              |  : |       | :| |      |     | :  |  | ||               ||
Db         77 LAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQ--CAQDRCNAKLNLTSRALDPAGNE---- 130

Qy        108 ENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGPMNQ----CLVATGTHEPKN--QSYMV 161
              | || :|||| | |    |       :: |    :      |      |   |  | |
Db        131 SAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTVSLPV 190

Qy        162 RGCATASMC-QHAHLGDAFSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHL 216
              |||      | :    |  |:::    |||  | ||    :  | |   |     | |
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Qy        217 SLTITLLMT 225
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Db        248 TVASTTSVT 256


RESULT 3
US-10-453-372-864
; Sequence 864, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-589 A
;  CURRENT APPLICATION NUMBER: US/10/453,372
;  CURRENT FILING DATE:  2003-06-03
;  PRIOR APPLICATION NUMBER: 09/789390
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 09/823187
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/195792
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 09/839446
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/199476
;  PRIOR FILING DATE: 2000-03-25
;  PRIOR APPLICATION NUMBER: 09/863776
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 60/208263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 09/939398
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/227800
;  PRIOR FILING DATE: 2000-08-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1609
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 864
;   LENGTH: 1418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-453-372-864

  Query Match             8.9%;  Score 116;  DB 6;  Length 1418;
  Best Local Similarity   21.8%;  Pred. No. 0.0034;
  Matches   62;  Conservative   24;  Mismatches   87;  Indels  112;  Gaps   16;

Qy         16 CVPASWGLRCM----QCKT-NGDCR----------------------------VEECAL 41
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Qy         42 GQDLC-----RTTIVR----------LWEEGEELELVEK--------SCTHSEKTNRTLS 78
              |   |     : || |           | |:|     | :         || |  :  | |:
Db        213 GNGGCQHHCVQLTITRHRCQCRPGFQLQEDGR--HCVRRSPCANRNGSCMHRCQVVRGLA 270

Qy         79 -------YR---TGLKITSLTEVVCGLDLCNQG--NSVLELE-------NLPQNGRQCY- 118
                    |:   |     : |   ||  |  |  |:    :         |  :|||||
Db        271 RCECHVGYQLAADGKACEDVDECAAGLAQCAHGCLNTQGSFKCVCHAGYELGADGRQCYR 330

Qy        119 -------SCKGNS---THGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATAS 168
                    ||: |:    :||||          ||:  |          :     |  || :
Db        331 IEMEIVNSCEANNGGCSHGCSHTSA------GPLCTCPRGYELDTDQRTCIDVGDCADSP 384

Qy        169 MCQH------------AHLG-----DAFSMNHIDVSCCTKSGCNH 196
                ||             : |     |      :|    :: ||| |
Db        385 CCQQVCTNNPGGYECGCYAGYRLSADGCGCEDVDECASSRGGCEH 429
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:07:51 ; Search time 4525.95 Seconds
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10964.406 Million cell updates/sec

Title: US-10-679-951-5
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_env:*
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5: gb_ov:*
6: gb_pat:*
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13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	873	100.0	1608	8	HSU08839	U08839 Human uroki
3	836.8	95.9	1609	6	AX281707	AX281707 Sequence
4	728	83.4	1008	6	AX663348	AX663348 Sequence
5	728	83.4	1008	11	AY893435	AY893435 Synthetic
6	728	83.4	1318	6	AX481417	AX481417 Sequence
7	728	83.4	1349	6	AR380630	AR380630 Sequence
8	728	83.4	1349	8	HUMMO3A	M83246 Human monoc
9	728	83.4	1353	8	BC002788	BC002788 Homo sapi
10	728	83.4	1363	6	AX787055	AX787055 Sequence
11	728	83.4	1363	8	HSUPARAA	X51675 H.sapiens u
12	728	83.4	1400	6	A18757	A18757 u-PA recept
13	728	83.4	1400	6	BD140440	BD140440 Urokinase
14	728	83.4	1400	6	BD188995	BD188995 Antibodie
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16	728	83.4	1407	6	I08456	I08456 Sequence 8
17	728	83.4	1740	6	CQ870630	CQ870630 Sequence
18	728	83.4	1743	6	CS050233	CS050233 Sequence
19	728	83.4	1743	6	AR659305	AR659305 Sequence
20	728	83.4	1745	6	AR659486	AR659486 Sequence
21	728	83.4	1883	6	CQ492946	CQ492946 Sequence
22	726.4	83.2	1008	11	AY893593	AY893593 Synthetic
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29	716.8	82.1	1107	8	AF302071	AF302071 Pan trogl
30	682.2	78.1	967	8	AF257789	AF257789 Homo sapi
31	681.6	78.1	1067	8	AF302073	AF302073 Macaca fa
32	680	77.9	1046	8	AF302072	AF302072 Cercopith
33	669.8	76.7	846	6	AX663342	AX663342 Sequence
34	625	71.6	952	8	AY029180	AY029180 Homo sapi
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36	539	61.7	711	6	AX663344	AX663344 Sequence
37	477	54.6	1097	6	AX770534	AX770534 Sequence
38	477	54.6	1097	8	HSUPAR	X74039 H.sapiens m
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ALIGNMENTS

RESULT 1
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LOCUS AX663346 873 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5 from Patent WO02082077.
ACCESSION AX663346
VERSION AX663346.1 GI:29163688
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
TITLE Production of polyclonal monospecific antibodies against upar variants del4, del5 and del4+5, and the use thereof for diagnostic and therapeutical purposes
JOURNAL Patent: WO 02082077-A 5 17-OCT-2002;
Wilex AG (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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/note="unnamed protein product"
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/db_xref="GI:29163689"
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ORIGIN

Query Match 100.0%; Score 873; DB 6; Length 873;
Best Local Similarity 100.0%; Pred. No. 6.4e-219;
Matches 873; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Db         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120

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Db        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180

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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Db        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300

Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420

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Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
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Db        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720

Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
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Db        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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RESULT 2
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LOCUS       HSU08839                1608 bp    mRNA    linear   PRI 30-JUL-1994
DEFINITION  Human urokinase-type plasminogen activator receptor mRNA, complete
            cds.
ACCESSION   U08839
VERSION     U08839.1  GI:517197
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Casey,J.R., Petranka,J.G., Kottra,J., Fleenor,D.E. and Rosse,W.F.
  TITLE     The Structure of the Urokinase-Type Plasminogen Activator Receptor
            Gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 381 to 1608)
  AUTHORS   Roldan,A.L., Cubellis,M.V., Masucci,M.T., Behrendt,N., Lund,L.R.,
            Dano,K., Appella,E. and Blasi,F.
  TITLE     Cloning and expression of the receptor for human urokinase
            plasminogen activator, a central molecule in cell surface, plasmin
            dependent proteolysis
  JOURNAL   EMBO J. 9 (2), 467-474 (1990)
   PUBMED   1689240
REFERENCE   3  (bases 1 to 1608)
  AUTHORS   Petranka,J.,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-1994) Petranka J. G., Duke University Medical
            Center, Hematology, South Hospital, Durham, NC 27710, USA
FEATURES             Location/Qualifiers
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                     /cell_line="HeLa"
                     /clone_lib="cDNA library"
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                     Number X51675"
     CDS             427. .1299
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ORIGIN
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  Query Match           100.0%;  Score 873;  DB 8;  Length 1608;
  Best Local Similarity  100.0%;  Pred. No. 6.4e-219;
  Matches  873;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Db        427 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 486

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
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Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
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Db        907 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 966

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
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Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
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Db       1027 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 1086

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
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Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
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Db       1147 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 1206

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
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Db       1207 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 1266

Qy        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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Db       1267 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1299


RESULT 3
AX281707
LOCUS       AX281707               1609 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 116 from Patent WO0177389.
ACCESSION   AX281707
VERSION     AX281707.1  GI:16608958
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
            Mikita,T. and Tai,J.
  TITLE     Genes expressed in foam cell differentiation
  JOURNAL   Patent: WO 0177389-A 116 18-OCT-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1609
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                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             95.9%;  Score 836.8;  DB 6;  Length 1609;
  Best Local Similarity   97.1%;  Pred. No. 2.2e-209;
  Matches  849;  Conservative    0;  Mismatches   24;  Indels    1;  Gaps    1;

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Qy        780 GGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGC 839
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Qy        840 CAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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RESULT 4
AX663348
LOCUS       AX663348               1008 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 7 from Patent WO02082077.
ACCESSION   AX663348
VERSION     AX663348.1  GI:29163690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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          Hominidae; Homo.
REFERENCE   1
  AUTHORS   Luther,T., Magdolen,V., Schmitt,M. and Muehlenweg,B.
  TITLE     Production of polyclonal monospecific antibodies against upar
            variants del4, del5 and del4+5, and the use thereof for diagnostic
            and therapeutical purposes
  JOURNAL   Patent: WO 02082077-A 7 17-OCT-2002;
            Wilex AG (DE)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             83.4%;  Score 728;  DB 6;  Length 1008;
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  Matches  873;  Conservative    0;  Mismatches    0;  Indels  135;  Gaps    1;

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Qy        473 ------------------------------------------------------------ 472

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Qy        473 -------TCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 525
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Db        601 GGCCCAATCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 660

Qy        526 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 585
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Db        661 GGGAACAGCACCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCC 720

Qy        586 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 645
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Qy        706 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 765
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Qy        826 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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Db        961 CTGCTAATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1008


RESULT 5
AY893435
LOCUS       AY893435               1008 bp    mRNA    linear   SYN 16-MAR-2005
DEFINITION  Synthetic construct Homo sapiens clone FLH127783.01X plasminogen
            activator urokinase receptor (PLAUR) mRNA, complete cds.
ACCESSION   AY893435
VERSION     AY893435.1  GI:60818642
KEYWORDS    Human ORF Project.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B.,
            Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
  TITLE     Cloning of human full-length CDS FLEXGene in
            Gateway(TM) recombinational vector system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B.,
            Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2005) Biological Chemistry and Molecular
            Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
            Cambridge, MA 02141, USA
COMMENT     This CDS clone is a part of a collection of human full-length
            expression clones generated by Harvard Institute of Proteomics.
            This ORF clone has been cloned with normalized stop-codon. AttB
            recombination sites have been added to either end of the ORF and
            directionally cloned using the Gateway cloning system into pDONR
            201. Additional sequences in the clone:  'ACC' before the 'ATG'
            (corresponding to ribosomal binding site and Kozak consensus
            sequences).  Each clone is clonally isolated and full-length
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FEATURES             Location/Qualifiers
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                     from placenta and brain"
     gene            1. .1008
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     CDS             1. .1008
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	873	100.0	1608	10	ABZ82961	Abz82961 Toxicolog
3	845	96.8	1601	11	ACN45051	Acn45051 Human mRN
4	836.8	95.9	1609	6	AAS94861	Aas94861 Human DNA
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6	728	83.4	1318	6	ABV78147	Abv78147 Human uro
7	728	83.4	1318	6	ABZ35723	Abz35723 Human UPA
8	728	83.4	1318	6	ABX09966	Abx09966 Human UPA
9	728	83.4	1318	6	ABL91688	Abl91688 Human pol
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21	728	83.4	1548	14	ADZ80553	Adz80553 Plasminog
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32	728	83.4	1883	5	ABV24824	Abv24824 Human pro
33	728	83.4	1887	12	ADQ23719	Adq23719 Human sof
34	723	82.8	1400	4	AAS12134	Aas12134 Human u-P
35	715.2	81.9	1400	2	ACA62905	Aca62905 cDNA enco
36	705.6	80.8	1400	2	AAX19823	Aax19823 Urokinase
37	701	80.3	1700	13	ACN43281	Acn43281 Human dia
38	698	80.0	1370	8	ABX34691	Abx34691 Human mdd
39	669.8	76.7	846	9	ABZ26096	Abz26096 Human uPA
40	625	71.6	952	13	ADR14422	Adr14422 Human NF-
41	573.6	65.7	1247	4	AAS12135	Aas12135 Human u-P
42	539	61.7	711	9	ABZ26097	Abz26097 Human uPA
43	477	54.6	1097	8	ACA89919	Aca89919 Gene diff
44	477	54.6	1097	12	ADP13365	Adp13365 Renal cel
45	453	51.9	483	6	ABK54730	Abk54730 Human col

ALIGNMENTS

RESULT 1
ABZ26098
ID ABZ26098 standard; cDNA; 873 BP.
XX
AC ABZ26098;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human uPAR exon 5 deletion variant encoding cDNA SEQ ID NO 5.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; GenBank Number U08839; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .846
FT /*tag= a
FT /product= "uPAR exon 5 deletion variant"
XX
PN DE10117381-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001DE-01017381.
XX
PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR P-PSDB; ABP60421.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 3; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a

```
CC   urokinase type plasminogen activator receptor (uPAR) which has one or two
CC   exons of the native sequence at least partly missing, excluding Genbank
CC   sequence U08839. Molecules of the invention are used to diagnose,
CC   prognose and treat cancer, particularly breast or ovarian cancer. The
CC   present sequence is that of a uPAR exon 5 deletion variant encoding cDNA
CC   (GenBank number U08839) of the invention
XX
SQ   Sequence 873 BP; 197 A; 256 C; 249 G; 171 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 873;  DB 9;  Length 873;
  Best Local Similarity  100.0%;  Pred. No. 7e-228;
  Matches  873;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300

Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360

Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420

Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480

Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720

Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840

Qy        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
              ||||||||||||||||||||||||||||||||
Db        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
```

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RESULT 2
ABZ82961/c
ID   ABZ82961 standard; cDNA; 1608 BP.
XX
AC   ABZ82961;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human nucleotide sequence #120.
XX
KW   Toxicologically relevant gene; toxicological response; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 90; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 1608 BP; 342 A; 443 C; 452 G; 371 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 873;  DB 10;  Length 1608;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-228;
  Matches  873;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1182 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 1123

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 1063
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 1003

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 943

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 883

Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 823

Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 763

Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 703

Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 643

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 583

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 523

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 463

Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 403

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 343

Qy        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
              ||||||||||||||||||||||||||||||||
Db        342 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 310
```

RESULT 3
ACN45051
ID ACN45051 standard; cDNA; 1601 BP.
XX
AC ACN45051;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human mRNA sequence hCT1950668.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 1805; 0pp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA gene
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 1601 BP; 369 A; 449 C; 442 G; 341 T; 0 U; 0 Other;

Query Match 96.8%; Score 845; DB 11; Length 1601;
Best Local Similarity 99.0%; Pred. No. 3.8e-220;
Matches 864; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

```
Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 487

Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 547

Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 607

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 667

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 727

Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 787

Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 847

Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 907

Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 967

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        968 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 1027

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
              ||||||||          ||||||||||||||||||||||||||||||||||||||||||
Db       1028 GTAGCCAC---------CGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 1078

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 1138

Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 1198

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 1258

Qy        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
              |||||||||||||||||||||||||||||||||
Db       1259 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1291


RESULT 4
AAS94861
ID   AAS94861 standard; DNA; 1609 BP.
XX
AC   AAS94861;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human DNA sequence #116 expressed during foam cell differentiation.
XX
KW   Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW   cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177389-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US011128.
XX
PR   05-APR-2000; 2000US-0195106P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Shiffman D,  Somogyi R,  Lawn R,  Seilhamer JJ,  Porter GJ,  Mikita T;
PI   Tai J;
XX
DR   WPI; 2002-010925/01.
XX
PT   Composition useful for diagnosis of conditions, disorders or diseases
PT   associated with atherosclerosis, comprises several polynucleotides that
PT   are differentially expressed in foam cell development.
XX
PS   Claim 1; Page 170-171; 315pp; English.
XX
CC   The present invention relates to the isolation of human polynucleotide
CC   sequences that are differentially expressed during foam cell
CC   differentiation. The polynucleotide sequences of the invention or a
CC   composition comprising these polynucleotides are useful as a high
CC   throughput method for detecting altered expression of one or more
CC   polynucleotides in a sample. The polynucleotides can be used in the
CC   diagnosis of disorders associated with foam cell development such as
CC   atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC   coronary artery disease. The polynucleotide sequences can also be used as
CC   PCR primers and probes. The polynucleotides of the invention are also
CC   useful in gene therapy. AAS94746-AAS95021 represent the human
CC   polynucleotide sequences of the invention which are differentially
CC   expressed during foam cell differentiation
XX

SQ   Sequence 1609 BP; 346 A; 396 C; 407 G; 303 T; 0 U; 157 Other;

  Query Match             95.9%;  Score 836.8;  DB 6;  Length 1609;
  Best Local Similarity   97.1%;  Pred. No. 6.7e-218;
  Matches  849;  Conservative    0;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 ATGGGTCACCCGCCGCTGC-TGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTC 59
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        427 ATGGGTCACCCGCCGCTGCNNNNNNNNNNNNNNNNNNNNNACACCTGCGTCCCAGCCTC 486

Qy         60 TTGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGC 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TTGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGC 546

Qy        120 CCTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCT 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCT 606

Qy        180 GGAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GGAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCG 666

Qy        240 GACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCA 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCA 726

Qy        300 GGGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTG 359
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Db        727 GGGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTG 786

Qy        360 TGGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCC 419
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Qy        420 TGAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGA 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TGAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGA 906

Qy        480 GCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCA 539
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Db        907 GCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCA 966

Qy        540 TGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCT 1026

Qy        600 GGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAAC 659
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Db       1027 GGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAAC 1086

Qy        660 CGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGT 719
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Db       1087 CGCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGT 1146

Qy        720 CTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGG 779
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Db       1147 CTCCTGCTGTACTAAAAGTGGCTGTAACCANCCAGACCTGGGTGTCCAGTACCGCAGTGG 1206

Qy        780 GGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGC 839
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
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Qy        840 CAGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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RESULT 5
ABZ26099
ID   ABZ26099 standard; cDNA; 1008 BP.
XX
AC   ABZ26099;
XX
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:10:21 ; Search time 3532.6 Seconds
(without alignments)
11562.352 Million cell updates/sec

Title: US-10-679-951-5
Perfect score: 873
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 873

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	802.2	91.9	1078	3	BM543893	BM543893 AGENCOURT
2	728	83.4	1008	11	DQ050301	DQ050301 Homo sapi
3	728	83.4	1303	4	CR606767	CR606767 full-leng
4	728	83.4	1320	4	CR611518	CR611518 full-leng
5	728	83.4	1348	4	CR591481	CR591481 full-leng
6	724	82.9	905	3	BI906745	BI906745 603064474
7	720	82.5	1008	11	DQ050302	DQ050302 Pan trogl
8	673	77.1	1724	4	CR601067	CR601067 full-leng
9	633	72.5	691	1	AL710258	AL710258 DKFZp686G
10	625.2	71.6	954	1	AL556275	AL556275
11	615	70.4	1145	3	BM922342	BM922342 AGENCOURT
12	614.8	70.4	1130	3	BM906800	BM906800 AGENCOURT
13	610.4	69.9	983	1	AL554548	AL554548
14	600	68.7	649	3	BM767461	BM767461 K-EST0049
15	559	64.0	765	6	CF126152	CF126152 UI-HF-ET0
16	536	61.4	841	8	DR760518	DR760518 HESC4_117
17	529.4	60.6	892	6	CA489863	CA489863 AGENCOURT
18	525.6	60.2	1082	3	BM546227	BM546227 AGENCOURT
19	519	59.5	972	5	BU163129	BU163129 AGENCOURT
20	513.4	58.8	968	1	AL554495	AL554495 AL554495
21	513.2	58.8	573	1	AA481379	AA481379 zv44g07.r
22	506.4	58.0	945	2	BG680145	BG680145 602626809
23	498.8	57.1	900	6	CA488827	CA488827 AGENCOURT
24	494	56.6	1030	3	BM914922	BM914922 AGENCOURT
25	482.4	55.3	811	7	CR975202	CR975202 CR975202
26	475.4	54.5	938	5	BQ918717	BQ918717 AGENCOURT
27	473.2	54.2	896	5	BQ691008	BQ691008 AGENCOURT
28	472	54.1	542	5	BX480409	BX480409 DKFZp686B
29	472	54.1	548	7	CN336454	CN336454 170004243
30	472	54.1	550	3	BP269193	BP269193 BP269193
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32	472	54.1	573	3	BP269195	BP269195 BP269195
33	472	54.1	579	3	BP268735	BP268735 BP268735
34	472	54.1	580	3	BP268736	BP268736 BP268736
35	472	54.1	580	3	BP299935	BP299935 BP299935
36	472	54.1	582	3	BP300192	BP300192 BP300192
37	472	54.1	582	3	BP301778	BP301778 BP301778
38	472	54.1	584	3	BP354862	BP354862 BP354862
39	472	54.1	605	2	BE386005	BE386005 601276664
40	472	54.1	628	5	BU785259	BU785259 in43b03.y
41	472	54.1	659	7	CN336456	CN336456 170006001
42	472	54.1	663	2	BF129898	BF129898 601817708
43	472	54.1	757	7	CR996305	CR996305 CR996305
44	472	54.1	776	6	CF126247	CF126247 UI-HF-ET0
45	472	54.1	778	3	BI910493	BI910493 603067865

ALIGNMENTS

RESULT 1
BM543893
LOCUS BM543893 1078 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6492429 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589238 5', mRNA sequence.
ACCESSION BM543893
VERSION BM543893.1 GI:18774681
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12361 row: j column: 23
High quality sequence start: 29
High quality sequence stop: 601.
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5589238"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 036."

ORIGIN

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  Query Match             91.9%;  Score 802.2;  DB 3;  Length 1078;
  Best Local Similarity   96.9%;  Pred. No. 6.9e-204;
  Matches  838;  Conservative    0;  Mismatches   25;  Indels    2;  Gaps    2;

Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
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Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
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Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
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Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
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Db        523 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 582

Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
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Db        583 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 642

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
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Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
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Db        822 GCTGCTCCCTCAGCCTGGCCCTGCCCATCTAAGCCTCACCATCACCCTTGCTATGACTGG 881

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Db        882 CAAAATTGGGGGGAAGGCCCTCTTC 906
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RESULT 2
DQ050301
LOCUS DQ050301 1008 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens PLAUR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ050301
VERSION DQ050301.1 GI:66903500
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1008)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
gene <1. .>1008
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/locus_tag="HC18297"

ORIGIN

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  Matches  873;  Conservative    0;  Mismatches    0;  Indels  135;  Gaps    1;

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Db        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGGGCGTCCA 480
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:24:01 ; Search time 176.756 Seconds
(without alignments)
8779.420 Million cell updates/sec

Title: US-10-679-951-5
Perfect score: 873
Sequence: 1 atgggtcacccgccgctgct.....gcactctcctctggacctaa 873

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	728	83.4	1400	2	US-08-085-122-12	Sequence 12, Appl
	3	728	83.4	1400	3	US-08-442-108B-22	Sequence 22, Appl
	4	728	83.4	1743	3	US-09-949-002-60	Sequence 60, Appl
	5	728	83.4	1745	3	US-09-949-002-241	Sequence 241, App
	6	255	29.2	25966	3	US-09-949-002-632	Sequence 632, App
	7	255	29.2	25966	3	US-09-949-002-813	Sequence 813, App
c	8	254.6	29.2	601	3	US-09-949-002-2319	Sequence 2319, Ap
c	9	254.6	29.2	601	3	US-09-949-002-9335	Sequence 9335, Ap
c	10	86	9.9	601	3	US-09-949-002-2317	Sequence 2317, Ap
c	11	86	9.9	601	3	US-09-949-002-9333	Sequence 9333, Ap
c	12	78.6	9.0	601	3	US-09-949-002-2307	Sequence 2307, Ap
c	13	78.6	9.0	601	3	US-09-949-002-9323	Sequence 9323, Ap
	14	50	5.7	50	3	US-10-131-827-2347	Sequence 2347, Ap
c	15	44.6	5.1	1651	3	US-09-902-540-3255	Sequence 3255, Ap
c	16	44.6	5.1	19954	3	US-09-902-540-1150	Sequence 1150, Ap
	17	43.6	5.0	1527	3	US-09-489-039A-716	Sequence 716, App
c	18	42	4.8	56	3	US-09-381-244B-24	Sequence 24, Appl
	19	39.6	4.5	3289	3	US-09-587-945-1	Sequence 1, Appli
	20	39.4	4.5	7847	3	US-09-799-451-591	Sequence 591, App
c	21	38	4.4	116955	3	US-09-949-016-17565	Sequence 17565, A
	22	37.6	4.3	601	3	US-09-949-016-206248	Sequence 206248,
c	23	37.2	4.3	1440	2	US-08-224-482-5	Sequence 5, Appli
c	24	37.2	4.3	2700	3	US-09-023-655-1069	Sequence 1069, Ap
c	25	37.2	4.3	2811	2	US-08-040-548-31	Sequence 31, Appl
c	26	37.2	4.3	2811	2	US-08-466-344-31	Sequence 31, Appl
c	27	37.2	4.3	2817	9	5206152-6	Patent No. 5206152
c	28	37.2	4.3	2887	3	US-09-964-899-34	Sequence 34, Appl
c	29	37.2	4.3	2977	3	US-09-919-039-65	Sequence 65, Appl
	30	36.8	4.2	432	3	US-09-060-299-5	Sequence 5, Appli
	31	36.8	4.2	432	3	US-09-402-923A-5	Sequence 5, Appli
	32	36.8	4.2	4843	3	US-09-060-299-2	Sequence 2, Appli
	33	36.8	4.2	4843	3	US-09-402-923A-2	Sequence 2, Appli
	34	36.8	4.2	5098	3	US-09-060-299-1	Sequence 1, Appli
	35	36.8	4.2	5098	3	US-09-402-923A-1	Sequence 1, Appli
	36	36.8	4.2	5103	3	US-09-949-016-2457	Sequence 2457, Ap
	37	36.8	4.2	5120	3	US-09-544-398B-1	Sequence 1, Appli
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c	45	36.2	4.1	337	3	US-09-324-542-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-09-023-655-1175
; Sequence 1175, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g188623

US-09-023-655-1175

Query Match 83.4%; Score 728; DB 3; Length 1349;
Best Local Similarity 86.6%; Pred. No. 1.1e-197;
Matches 873; Conservative 0; Mismatches 0; Indels 135; Gaps 1;

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Qy        766 CAGTACCGCAGTGGGGCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACC 825
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RESULT 2
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; Sequence 12, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..1054
US-08-085-122-12

Query Match 83.4%; Score 728; DB 2; Length 1400;
Best Local Similarity 86.6%; Pred. No. 1.1e-197;
Matches 873; Conservative 0; Mismatches 0; Indels 135; Gaps 1;

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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	873	100.0	873	8	US-10-679-951-5	Sequence 5, Appli
2	845	96.8	1601	5	US-10-087-192-1805	Sequence 1805, Ap
3	836.8	95.9	1609	6	US-10-240-965-116	Sequence 116, App
4	728	83.4	1008	8	US-10-679-951-7	Sequence 7, Appli
5	728	83.4	1318	7	US-10-384-339C-31	Sequence 31, Appl
6	728	83.4	1349	7	US-10-641-643-1175	Sequence 1175, Ap
7	728	83.4	1363	5	US-10-193-656-5	Sequence 5, Appli
8	728	83.4	1740	8	US-10-783-528-39	Sequence 39, Appl
9	728	83.4	1743	6	US-10-177-293-361	Sequence 361, App
10	728	83.4	1743	6	US-10-172-118-799	Sequence 799, App
11	728	83.4	1743	6	US-10-388-360-372	Sequence 372, App
12	728	83.4	1743	6	US-10-295-027-1110	Sequence 1110, Ap
13	728	83.4	1743	7	US-10-429-160-74	Sequence 74, Appl
14	728	83.4	1743	7	US-10-342-887-799	Sequence 799, App
15	728	83.4	1743	8	US-10-723-860-2343	Sequence 2343, Ap
16	728	83.4	1883	8	US-10-357-930-24813	Sequence 24813, A
17	728	83.4	1887	8	US-10-723-860-6539	Sequence 6539, Ap
18	669.8	76.7	846	8	US-10-679-951-1	Sequence 1, Appli
19	625	71.6	952	7	US-10-755-889-423	Sequence 423, App
20	539	61.7	711	8	US-10-679-951-3	Sequence 3, Appli
21	477	54.6	1097	7	US-10-240-425-1547	Sequence 1547, Ap
22	477	54.6	1097	7	US-10-717-597-101	Sequence 101, App
23	453	51.9	483	3	US-09-919-580-200	Sequence 200, App
24	378.4	43.3	419	3	US-09-918-995-35682	Sequence 35682, A
25	357.4	40.9	539	7	US-10-283-975A-24	Sequence 24, Appl
26	255	29.2	739	3	US-09-962-832-120	Sequence 120, App
27	255	29.2	739	8	US-10-482-029-159	Sequence 159, App
28	255	29.2	739	9	US-10-843-641A-6006	Sequence 6006, Ap
29	255	29.2	41966	5	US-10-087-192-1804	Sequence 1804, Ap
30	239.6	27.4	1272	7	US-10-152-319A-1705	Sequence 1705, Ap
31	234	26.8	431	8	US-10-357-930-37459	Sequence 37459, A
32	231.2	26.5	984	5	US-10-087-192-1802	Sequence 1802, Ap
33	168.8	19.3	275	8	US-10-357-930-7499	Sequence 7499, Ap
c 34	150	17.2	521	6	US-10-029-386-7358	Sequence 7358, Ap
c 35	147	16.8	148	6	US-10-029-386-21058	Sequence 21058, A
36	143.8	16.5	409	3	US-09-813-358-205	Sequence 205, App
37	143.8	16.5	409	3	US-09-997-279-205	Sequence 205, App
c 38	117	13.4	561	6	US-10-029-386-11796	Sequence 11796, A
c 39	111	12.7	112	6	US-10-029-386-25496	Sequence 25496, A
40	104	11.9	406	5	US-10-066-543-1724	Sequence 1724, Ap
41	104	11.9	406	5	US-10-066-543-2399	Sequence 2399, Ap
42	102.2	11.7	147	8	US-10-425-115-118390	Sequence 118390,
43	88.6	10.1	32963	5	US-10-087-192-1801	Sequence 1801, Ap
44	76	8.7	76	8	US-10-714-195-72	Sequence 72, Appl
45	76	8.7	76	9	US-10-852-797-352	Sequence 352, App

ALIGNMENTS

RESULT 1
US-10-679-951-5
; Sequence 5, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-679-951-5

Query Match 100.0%; Score 873; DB 8; Length 873;
Best Local Similarity 100.0%; Pred. No. 9.7e-267;
Matches 873; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360

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Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
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Db        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480

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Db        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540

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RESULT 2
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; Sequence 1805, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1805
;   LENGTH: 1601
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-087-192-1805

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Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
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Db        728 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 787

Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
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Db        788 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 847

Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 480
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Db        848 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGTCCTGGAG 907

Qy        481 CTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 600
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Db        968 GGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTG 1027

Qy        601 GTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 660
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Db       1028 GTAGCCAC---------CGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACC 1078

Qy        661 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 GCCTCAATGTGCCAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTC 1138

Qy        721 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 TCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGG 1198

Qy        781 GCTGCTCCTCAGCCTGGCCCTGCCCATCTCAGCCTCACCATCACCCTGCTAATGACTGCC 840
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Qy        841 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 873
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Db       1259 AGACTGTGGGGAGGCACTCTCCTCTGGACCTAA 1291


RESULT 3
US-10-240-965-116
; Sequence 116, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  SHIFFMAN, Dov
;  APPLICANT:  SOMOGYI, Roland
;  APPLICANT:  LAWN, Richard M.
;  APPLICANT:  SEILHAMER, Jeffrey J.
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 21:56:22 ; Search time 383.689 Seconds
(without alignments)
1875.453 Million cell updates/sec

Title: US-10-679-951-5
Perfect score: 873
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	728	83.4	1743	6	US-10-826-585-57	Sequence 57, Appl
	2	268.8	30.8	972	8	US-11-128-061-722	Sequence 722, App
	3	268.8	30.8	972	8	US-11-128-049-722	Sequence 722, App
	4	239.6	27.4	1277	8	US-11-136-527-2432	Sequence 2432, Ap
	5	169.2	19.4	600	8	US-11-128-061-4364	Sequence 4364, Ap
	6	169.2	19.4	600	8	US-11-128-049-4364	Sequence 4364, Ap
	7	122.4	14.0	600	8	US-11-136-527-6528	Sequence 6528, Ap
	8	39.6	4.5	1506	7	US-10-971-560-9	Sequence 9, Appli
	9	39.6	4.5	3289	7	US-10-971-560-8	Sequence 8, Appli
	10	39.6	4.5	4158	7	US-10-971-560-3	Sequence 3, Appli
	11	39.6	4.5	6458	7	US-10-971-560-1	Sequence 1, Appli
	12	36.8	4.2	5100	8	US-11-108-528-79	Sequence 79, Appl
c	13	36.2	4.1	552	8	US-11-055-637-98	Sequence 98, Appl
c	14	35.4	4.1	4663	7	US-10-995-561-435	Sequence 435, App
c	15	35.4	4.1	67126	7	US-10-995-561-13342	Sequence 13342, A
c	16	35.2	4.0	201	7	US-10-995-561-11403	Sequence 11403, A
c	17	35.2	4.0	201	7	US-10-995-561-59208	Sequence 59208, A
	18	34	3.9	649	7	US-10-516-768-7	Sequence 7, Appli
	19	33.6	3.8	3703	7	US-10-750-185-27363	Sequence 27363, A
	20	33.6	3.8	3703	7	US-10-750-623-27363	Sequence 27363, A
	21	33.6	3.8	5119	8	US-11-108-528-81	Sequence 81, Appl
	22	33.4	3.8	1625	7	US-10-750-185-43394	Sequence 43394, A
	23	33.4	3.8	1625	7	US-10-750-623-43394	Sequence 43394, A
c	24	33	3.8	1156	7	US-10-750-185-26927	Sequence 26927, A
c	25	33	3.8	1156	7	US-10-750-623-26927	Sequence 26927, A
c	26	33	3.8	1662	8	US-11-136-619-3	Sequence 3, Appli
c	27	32.6	3.7	1332	7	US-10-967-648A-7	Sequence 7, Appli
	28	32.6	3.7	157224	8	US-11-112-908-51	Sequence 51, Appl
	29	32.6	3.7	161726	8	US-11-112-908-48	Sequence 48, Appl
	30	32.6	3.7	161726	8	US-11-112-908-52	Sequence 52, Appl
	31	32.6	3.7	170189	8	US-11-112-908-50	Sequence 50, Appl
c	32	32.4	3.7	1684	7	US-10-750-185-29991	Sequence 29991, A
c	33	32.4	3.7	1684	7	US-10-750-623-29991	Sequence 29991, A
c	34	32.2	3.7	1305	7	US-10-750-185-61512	Sequence 61512, A
c	35	32.2	3.7	1305	7	US-10-750-623-61512	Sequence 61512, A
c	36	32	3.7	444	8	US-11-136-527-1083	Sequence 1083, Ap
c	37	32	3.7	444	8	US-11-136-527-5179	Sequence 5179, Ap
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c	39	32	3.7	951	7	US-10-750-623-32051	Sequence 32051, A
c	40	32	3.7	1162	7	US-10-750-185-48518	Sequence 48518, A
c	41	32	3.7	1162	7	US-10-750-623-48518	Sequence 48518, A
	42	32	3.7	4564	7	US-10-750-185-63324	Sequence 63324, A
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c	44	31.8	3.6	1558	7	US-10-995-561-70	Sequence 70, Appl
c	45	31.8	3.6	1644	7	US-10-995-561-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-10-826-585-57
; Sequence 57, Application US/10826585
; Publication No. US20060008807A1
; GENERAL INFORMATION:
; APPLICANT: Immunivest Corporation
; APPLICANT: O'Hara, Shawn Mark
; APPLICANT: Foulk, Brad
; APPLICANT: Zweitzig, Daniel
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
; TITLE OF INVENTION: morphological features on the same sample
; FILE REFERENCE: IMMC 143 PCT/US
; CURRENT APPLICATION NUMBER: US/10/826,585
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/369945
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/330669
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/26867
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Human
US-10-826-585-57

Query Match 83.4%; Score 728; DB 6; Length 1743;
Best Local Similarity 86.6%; Pred. No. 1.7e-194;
Matches 873; Conservative 0; Mismatches 0; Indels 135; Gaps 1;

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Qy          1 ATGGGTCACCCGCCGCTGCTGCCGCTGCTGCTGCTGCTCCACACCTGCGTCCCAGCCTCT 60
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Qy         61 TGGGGCCTGCGGTGCATGCAGTGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCC 120
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Qy        121 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 180
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Db        547 CTGGGACAGGACCTCTGCAGGACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTG 606

Qy        181 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 240
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Db        607 GAGCTGGTGGAGAAAAGCTGTACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGG 666

Qy        241 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 300
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Db        667 ACTGGCTTGAAGATCACCAGCCTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAG 726

Qy        301 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 360
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Db        727 GGCAACTCTGGCCGGGCTGTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGT 786

Qy        361 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 420
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Db        787 GGCTCATCAGACATGAGCTGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCT 846

Qy        421 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAG-------- 472
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 GAAGAACAGTGCCTGGATGTGGTGACCCACTGGATCCAGGAAGGTGAAGAAGGGCGTCCA 906

Qy        473 ---------------------------------------------------------- 472

Db        907 AAGGATGACCGCCACCTCCGTGGCTGTGGCTACCTTCCCGGCTGCCCGGGCTCCAATGGT 966

Qy        473 ---------------------------------------------------------- 472

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Qy        473 -------TCCTGGAGCTTGAAAATCTGCCGCAGAATGGCCGCCAGTGTTACAGCTGCAAG 525
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Qy        586 ATGAATCAATGTCTGGTAGCCACCGGCACTCACGAACCGAAAAACCAAAGCTATATGGTA 645
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Qy        706 AACCACATTGATGTCTCCTGCTGTACTAAAAGTGGCTGTAACCACCCAGACCTGGATGTC 765
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RESULT 2
US-11-128-061-722
; Sequence 722, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 722
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-722

Query Match 30.8%; Score 268.8; DB 8; Length 972;
Best Local Similarity 60.4%; Pred. No. 1.1e-65;
Matches 591; Conservative 0; Mismatches 237; Indels 150; Gaps 3;

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Db         16 CCGCCGCTGCTGCTGCTGCTCGCCTGGGCCCCAGCCTCCCCGGGCCTGCGGTGCATGCAG 75

Qy         82 TGTAAGACCAACGGGGATTGCCGTGTGGAAGAGTGCGCCCTGGGACAGGACCTCTGCAGG 141
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Qy        142 ACCACGATCGTGCGCTTGTGGGAAGAAGGAGAAGAGCTGGAGCTGGTGGAGAAAAGCTGT 201
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Db        136 ACCACTGTGCTTCATGAATGGGAAGATGATAACGAACTGGAGTTGGAGATGAGAGACTGC 195

Qy        202 ACCCACTCAGAGAAGACCAACAGGACCCTGAGCTATCGGACTGGCTTGAAGATCACCAGC 261
                |||| |  ||||| |||||||||||| ||||||||||   ||  ||||||| ||||
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Qy        262 CTTACCGAGGTTGTGTGTGGGTTAGACTTGTGCAACCAGGGCAACTCTGG---CCGGGCT 318
                ||  ||||||| |||||||     |||| | ||||||  |   |   ||||   ||| |
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Qy        319 GTCACCTATTCCCGAAGCCGTTACCTCGAATGCATTTCCTGTGGCTCATCAGACATGAGC 378
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Qy        379 TGTGAGAGGGGCCGGCACCAGAGCCTGCAGTGCCGCAGCCCTGAAGAACAGTGCCTGGAT 438
                |||||||||||||| | |||||||||| |||||    ||  | |||||||||  | ||
Db        376 TGTGAGAGGGGCCGGGAGCAGAGCCTGCAATGCCGCTATCCCGGAGAACAGTGTGTTGAG 435

Qy        439 GTGGTGACCCACTGGATCCAGGAA---------------------------------- 462
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Db        436 GTGGTCACCCTACGGAGCACGGAAAGGAGTCTGAAGGATGAGAACTACACCAGAGGCTGT 495

Qy        463 ---------------------------------------------------------- 462

Db        496 GGCAGTCTTCCCGGGTGCCCGGGCATAGCCGGTTTCCATGGCAACCACACCTTCCACTTC 555

Qy        463 ----------------------------GGTGAAGAAGTCCTGGAGCTTGAAAATCTG 492
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Db        556 CTGAGATGCTGCAACTCCACCCACTGCAATGGCGGCCCAGTTCTAAATCTTCGGGACTTA 615

Qy        493 CCGCAGAATGGCCGCCAGTGTTACAGCTGCAAGGGGAACAGCACCCATGGATGCTCCTCT 552
                || | |||||||  |||||||||||||||| |||| |||||||||| || || |||||
Db        616 CCACCGAATGGCGTCCAGTGTTACAGCTGCGAGGGCAACAGCACCCACGGGTGTTCCTCC 675

Qy        553 GAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTGGTAGCCACCGGC 612
                 |||||||| |||| |||||||||| || || ||| |||| || ||||  |||||||||
Db        676 AAAGAGACTTCCCTCGTTGACTGCCGGGGACCGATGGATCAGTGCCTGGAGGCCACCGGC 735

Qy        613 ACTCACGAACCGAAAAACCAAAGCTATATGGTAAGAGGCTGTGCAACCGCCTCAATGTGC 672
                  | | | |||||  ||  | |  || |||||||  | || || ||    ||||
Db        736 TTGGATGTGCTGGCAAACCGGAGTCACACCGTGAGAGGCTGCTCGACGGCTTCCTGGTGC 795

Qy        673 CAACATGCCCACCTGGGTGACGCCTTCAGCATGAACCACATTGATGTCTCCTGCTGTACT 732
                | |    ||||  |||  || ||||||  | ||| ||||     |  |||| ||||||  |
Db        796 CCAGGCTCCCATGTGGCAGATGCCTTCCTCCTGAGCCACCCCAACATCTCGTGCTGTGAT 855

Qy        733 AAAAGTGGCTGTAACCACCCAGACCTGGATGTCCAGTACCGCAGTGGGGCTGCTCCTCAG 792
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:03 ; Search time 76.5427 Seconds
(without alignments)
1664.689 Million cell updates/sec

Title: US-10-679-951-6
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	1568.5	97.9	335	2	AAR07561	Aar07561 Recombina
5	1568.5	97.9	335	2	AAR44424	Aar44424 Human pho
6	1568.5	97.9	335	2	AAR58707	Aar58707 Human pho
7	1568.5	97.9	335	2	AAR97612	Aar97612 Human uro
8	1568.5	97.9	335	2	AAW31165	Aaw31165 Human pho
9	1568.5	97.9	335	4	AAU04454	Aau04454 Human uro
10	1568.5	97.9	335	6	AAE37129	Aae37129 Human uro
11	1568.5	97.9	335	6	ABR47562	Abr47562 Breast ca
12	1568.5	97.9	335	6	ABP60422	Abp60422 Human uPA
13	1568.5	97.9	335	7	ADN40009	Adn40009 Cancer/an
14	1568.5	97.9	335	8	ADJ45544	Adj45544 LXR-ligan
15	1568.5	97.9	335	8	ADO47984	Ado47984 Human uro
16	1568.5	97.9	335	8	ADP12460	Adp12460 Protein e
17	1568.5	97.9	335	8	ADQ19525	Adq19525 Human sof
18	1568.5	97.9	335	8	ADP24414	Adp24414 PRO polyp
19	1568.5	97.9	335	8	ADR46684	Adr46684 Cancer-as
20	1563.5	97.6	335	2	ABU10413	Abu10413 Human uro
21	1561.5	97.5	335	2	AAY04103	Aay04103 Urokinase
22	1557.5	97.2	335	4	AAU07610	Aau07610 Human u-P
23	1555.5	97.1	335	3	AAB26241	Aab26241 Human uro
24	1539.5	96.1	330	9	AEB54709	Aeb54709 Human pla
25	1495.5	93.4	359	6	ABU11701	Abu11701 Human MDD
26	1385.5	86.5	301	8	ADR14423	Adr14423 Human NF-
27	1376.5	85.9	299	4	AAU07611	Aau07611 Human u-P
28	1314	82.0	286	8	ABM84629	Abm84629 Human dia
29	1293.5	80.7	281	6	ABP60419	Abp60419 Human uPA
30	1281.5	80.0	283	8	ADU73621	Adu73621 Urokinase
31	1281.5	80.0	283	9	AEA35322	Aea35322 Human mat
32	1268	79.2	236	6	ABP60420	Abp60420 Human uPA
33	1106.5	69.1	281	6	ABU89746	Abu89746 Protein d
34	879.5	54.9	327	7	ABM85796	Abm85796 Mouse pro
35	741	46.3	174	1	AAP60435	Aap60435 Sequence
36	741	46.3	174	2	AAR44423	Aar44423 Peptide c
37	741	46.3	174	2	AAR58710	Aar58710 Human PIP
38	741	46.3	174	2	AAW31168	Aaw31168 hPIP part
39	515	32.1	90	2	ABU10417	Abu10417 Human uro
40	515	32.1	90	2	AAY04101	Aay04101 Urokinase
41	515	32.1	90	4	AAU04458	Aau04458 Human u-P
42	493	30.8	92	2	AAW99896	Aaw99896 Urokinase
43	493	30.8	92	4	AAU04456	Aau04456 Human u-P
44	485	30.3	92	2	ABU10415	Abu10415 Human uro
45	280	17.5	94	1	AAP60434	Aap60434 Sequence

ALIGNMENTS

RESULT 1
ABP60421
ID ABP60421 standard; protein; 290 AA.
XX
AC ABP60421;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human uPAR exon 5 deletion variant protein SEQ ID NO 6.
XX
KW Human; urokinase type plasminogen activator receptor; uPAR; cytostatic;
KW cancer; receptor.
XX
OS Homo sapiens.
XX
PN DE10117381-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001DE-01017381.
XX
PR 06-APR-2001; 2001DE-01017381.
XX
PA (WILE-) WILEX BIOTECHNOLOGY GMBH.
XX
PI Luther T, Magdolen V, Schmitt M, Muehlenweg B;
XX
DR WPI; 2003-168688/17.
DR N-PSDB; ABZ26098.
XX
PT New nucleic acid encoding a deletion variant of a urokinase receptor
PT which has one of two exons missing, is useful to detect and treat cancer,
PT particularly breast and ovarian cancer.
XX
PS Disclosure; Fig 3; 28pp; German.
XX
CC The invention relates to a nucleic acid encoding a deletion variant of a
CC urokinase type plasminogen activator receptor (uPAR) which has one or two
CC exons of the native sequence at least partly missing, excluding Genbank
CC sequence U08839. Molecules of the invention are used to diagnose,
CC prognose and treat cancer, particularly breast or ovarian cancer. The
CC present sequence is that of a uPAR exon 5 deletion variant protein of the
CC invention
XX
SQ Sequence 290 AA;

Query Match 100.0%; Score 1602; DB 6; Length 290;

```
  Best Local Similarity   100.0%;  Pred. No. 1.7e-116;
  Matches  290;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180

Qy        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240

Qy        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
```

RESULT 2
ABM85797
ID ABM85797 standard; protein; 287 AA.
XX
AC ABM85797;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein sequence hCP1752538.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 5; SEQ ID NO 1806; 0pp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CAP. Note:
CC This patent is an equivalent to basic patent US2002182586A1, for which no
CC sequence data was published
XX
SQ Sequence 287 AA;

```
  Query Match             98.1%;  Score 1571.5;  DB 7;  Length 287;
  Best Local Similarity   99.0%;  Pred. No. 3.9e-114;
  Matches  287;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180

Qy        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db        181 GCSSEETFLIDCRGPMNQCLVAT---EPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 237

Qy        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 287
```

RESULT 3
AAP60436
ID AAP60436 standard; protein; 335 AA.
XX
AC AAP60436;
XX
DT 25-JUN-1991 (first entry)
XX
DE Sequence of human phospholipase inhibitory protein (hPIP) encoded by pLE-
DE 1.
XX
KW Anti-inflammatory; phospholipase inhibitor; inflammatory disorder;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO8606100-A.
XX
PD 23-OCT-1986.
XX
PF 14-APR-1986; 86WO-US000772.
XX
PR 15-APR-1985; 85US-00723046.
XX
PA (BIOT-) BIOTECHN RES PARTN.
XX
PI Johnson LF, Longenecke J;
XX
DR WPI; 1986-291667/44.
DR N-PSDB; AAN60374.
XX
PT Human antiinflammatory phospholipase inhibitor protein - obtd. by
PT purificn. of human inter:peritoneal dialysis fluid.
XX
PS Claim 2; Fig 13; 61pp; English.
XX
CC Lambda U200 was used to probe cDNA libraries for hPIP. Lambda U200 and
CC lambda U500 share approximately 50 bp at the 5' ends of each and then
CC diverge. This divergence was due to intron splicing. PMN600 not only
CC shares the 50 bp segment common to lambda U200 and lambda U500, but its
CC homology with lambda U500 extends for another approximately 200 bp. These
CC sequences then also diverge. This divergence was shown to be due to the
CC presence of optional 3' terminal exons in the gene. pLE-1 contains the
CC full-length coding sequence for hPIP. The hPIP can be used for producing
CC antibodies (claimed). The PIP proteins show in vitro activity as
CC phospholipase inihibitors. The proteins are useful both to control
CC inflammatory responses and to treat inflammatory disorders

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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:58 ; Search time 12.9368 Seconds
(without alignments)
2156.859 Million cell updates/sec

Title: US-10-679-951-6
Perfect score: 1602
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1568.5	97.9	335	2	A39743	u-plasminogen acti
2	1106.5	69.1	281	2	S39495	u-plasminogen acti
3	938	58.6	330	1	JN0561	urokinase-type pla
4	879.5	54.9	327	2	A55356	urokinase-type pla
5	861	53.7	328	2	S42152	urinary plasminoge
6	495.5	30.9	222	2	B41643	urokinase-type pla
7	495.5	30.9	222	2	B55356	urokinase-type pla
8	122.5	7.6	2180	2	T29764	hypothetical prote
9	122	7.6	1548	2	S34583	serine proteinase
10	122	7.6	2907	2	A57278	fibrillin-2 precur
11	122	7.6	2918	2	A54105	fibrillin-2 precur
12	115	7.2	909	1	QRXLL1	LDL receptor 1 pre
13	114	7.1	1018	2	T19693	hypothetical prote
14	112.5	7.0	2471	2	A49128	cell-fate determin
15	112	7.0	1620	2	T27283	hypothetical prote
16	111	6.9	1203	2	A49175	Motch B protein -
17	108	6.7	1574	2	T13954	MEGF6 protein - ra
18	107.5	6.7	601	2	D89711	protein F40E10.4 [
19	107.5	6.7	601	2	T22025	hypothetical prote
20	107	6.7	770	2	S04847	leukocyte adhesion
21	107	6.7	771	2	A45839	leukocyte adhesion
22	106.5	6.6	996	2	JE0237	apolipoprotein E r
23	106.5	6.6	2524	2	A35844	Xotch protein - Af
24	105.5	6.6	339	2	B34895	transcription fact
25	105.5	6.6	518	2	JC7387	testis-abundant fi
26	105.5	6.6	4543	1	A53102	alpha-2-macroglobu
27	105	6.6	925	2	T37475	lipoprotein recept
28	104.5	6.5	741	2	T46488	hypothetical prote
29	104.5	6.5	2090	2	T30075	hypothetical prote
30	104.5	6.5	2153	2	T30074	hypothetical prote
31	103.5	6.5	601	2	B36346	fibulin 1 precurso
32	103.5	6.5	683	2	C36346	fibulin 1 precurso
33	103.5	6.5	1737	2	T00209	MEGF8 protein - hu
34	103.5	6.5	2813	1	VWHU	von Willebrand fac
35	103	6.4	909	1	QRXLL2	LDL receptor 2 pre
36	103	6.4	1474	2	D88550	protein ZC84.6 [im
37	102.5	6.4	1046	2	A26838	prestalk protein p
38	102	6.4	185	1	JC2394	phospholipase A2 i
39	101.5	6.3	873	1	QRRBVD	VLDL receptor prec
40	101.5	6.3	1798	2	S53869	laminin beta-2 cha
41	101	6.3	18	2	I52614	u-plasminogen acti
42	101	6.3	1111	2	T26972	hypothetical prote
43	100.5	6.3	1217	1	EGMSMG	epidermal growth f
44	100.5	6.3	1584	2	T00026	brain-specific ang
45	100.5	6.3	1712	2	A38261	masking protein pr

ALIGNMENTS

RESULT 1
A39743
u-plasminogen activator receptor form 1 precursor - human
N;Alternate names: monocyte activation antigen Mo3; urokinase-type plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: S12376; A39743; A35242; S34461; I56138; S67529; I39206
R;Roldan, A.L.; Cubellis, M.V.; Masucci, M.T.; Behrendt, N.; Lund, L.R.; Dano, K.; Appel
EMBO J. 9, 467-474, 1990
A;Title: Cloning and expression of the receptor for human urokinase plasminogen activato
A;Reference number: S12376; MUID:90151622; PMID:1689240
A;Accession: S12376
A;Molecule type: mRNA
A;Residues: 1-335 <ROL>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:X51675; NID:g37604; PIDN:CAA35981.1; PID:g
R;Behrendt, N.; Ploug, M.; Patthy, L.; Houen, G.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 7842-7847, 1991
A;Title: The ligand-binding domain of the cell surface receptor for urokinase-type plasm
A;Reference number: A39743; MUID:91210310; PMID:1850423
A;Accession: A39743
A;Molecule type: protein
A;Residues: 23-24,'X',26-27,'XX',30-33,'X',35-38,'X',40,'X',42;110-116,'XX',119,'X' <BEH
A;Cross-references: UNIPARC:UPI00001770BD; UNIPARC:UPI00001770BE
R;Behrendt, N.; Ronne, E.; Ploug, M.; Petri, T.; Lober, D.; Nielsen, L.S.; Schleuning, W
J. Biol. Chem. 265, 6453-6460, 1990
A;Title: The human receptor for urokinase plasminogen activator. NH-2-terminal amino aci
A;Reference number: A35242; MUID:90202929; PMID:2156852
A;Accession: A35242
A;Molecule type: protein
A;Residues: 23,'X',25-38,'H',40-43,'X',45,'X',47-51,'X' <BE2>
A;Cross-references: UNIPARC:UPI0000143F2B
A;Note: the authors show a tentative identification of His for residue 39
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase p
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34461
A;Molecule type: mRNA
A;Residues: 246-335 <PYK>
A;Cross-references: UNIPARC:UPI00001770BF
R;Ploug, M.; Ronne, E.; Behrendt, N.; Jensen, A.L.; Blasi, F.; Dano, K.
J. Biol. Chem. 266, 1926-1933, 1991
A;Title: Cellular receptor for urokinase plasminogen activator. Carboxyl-terminal proces
A;Reference number: A38677; MUID:91107700; PMID:1846368
A;Contents: annotation
R;Min, H.Y.; Semnani, R.; Mizukami, I.F.; Watt, K.; Todd, R.F.
J. Immunol. 148, 3636-3642, 1992
A;Title: cDNA for Mo3, a monocyte activation antigen, encodes the human receptor for uro
A;Reference number: I56138; MUID:92268511; PMID:1316922
A;Accession: I56138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

```
A;Residues: 1-335 <RES>
A;Cross-references: UNIPARC:UPI000000D8C1; GB:M83246; NID:g188623; PIDN:AAA59862.1; PID:
R;Wang, Y.; Dang, J.; Johnson, L.K.; Selhamer, J.J.; Doe, W.F.
Eur. J. Biochem. 227, 116-122, 1995
A;Title: Structure of the human urokinase receptor gene and its similarity to CD59 and t
A;Reference number: S67529; MUID:95154279; PMID:7531640
A;Accession: S67529
A;Molecule type: DNA
A;Residues: 1-335 <WAN>
A;Cross-references: UNIPARC:UPI000000D8C1
A;Note: the authors translated the codon CGC for residue 51 as Ala
R;Casey, J.R.; Petranka, J.G.; Kottra, J.; Fleenor, D.E.; Rosse, W.F.
Blood 84, 1151-1156, 1994
A;Title: The structure of the urokinase-type plasminogen activator receptor gene.
A;Reference number: I39206; MUID:94325556; PMID:8049431
A;Accession: I39206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <RE2>
A;Cross-references: UNIPARC:UPI000000D8C1; EMBL:U09937; NID:g533374; PIDN:AAB60690.1; PI
C;Genetics:
A;Gene: uPAR
A;Introns: 19/1; 56/1; 104/1; 158/1; 203/1; 252/1
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; glycoprotein; membrane protein; phosphatidylinositol l
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-304/Product: (or 23-305 or 23-306) u-plasminogen activator receptor #status experim
F;23-107/Domain: Ly-6 homology <LY6A>
F;115-206/Domain: Ly-6 homology <LY6B>
F;214-301/Domain: Ly-6 homology <LY6C>
F;74,184,194,222,255/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             97.9%;  Score 1568.5;  DB 2;  Length 335;
  Best Local Similarity   86.3%;  Pred. No. 1.2e-110;
  Matches  289;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEE---------------------- 157
              ||||||||||||||||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        158 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 195
                                   :|||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        196 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

Qy        256 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
              ||||||||||||||||||||||||||||||||||
Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 2
S39495
u-plasminogen activator receptor form 2 precursor - human
N;Alternate names: urokinase-type plasminogen activator receptor form 2
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S39495; S34462
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; D
submitted to the EMBL Data Library, December 1993
A;Description: An alternatively spliced variant of mRNA for the human receptor for uroki
A;Reference number: S39495
A;Accession: S39495
A;Molecule type: mRNA
A;Residues: 1-281 <PYK1>
A;Cross-references: UNIPROT:Q03405; UNIPARC:UPI000002B696; EMBL:X74039; NID:g456192; PIDN
R;Pyke, C.; Eriksen, J.; Solberg, H.; Schnack Nielsen, B.; Kristensen, P.; Lund, L.R.; Da
FEBS Lett. 326, 69-74, 1993
A;Title: An alternatively spliced variant of mRNA for the human receptor for urokinase pl
A;Reference number: S34461; MUID:93314820; PMID:8392005
A;Accession: S34462
A;Molecule type: mRNA
A;Residues: 246-281 <PYK2>
A;Cross-references: UNIPARC:UPI000016A0A4; GB:U09347; GB:S63673; NID:g483827; PIDN:AAA179
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: alternative splicing; receptor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-281/Product: u-plasminogen activator receptor #status predicted <MAT>
F;115-206/Domain: Ly-6 homology <LY6>

  Query Match             69.1%;  Score 1106.5;  DB 2;  Length 281;
  Best Local Similarity   81.7%;  Pred. No. 5.1e-76;
  Matches  206;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEE---------------------- 157
              ||||||||||||||||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEGRPKDDRHLRGCGYLPGCPGSNG 180

Qy        158 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 195
                                   :|||||||||||||||||||||||||||||||||||||
Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        196 MNQCLVATGTHE 207
              ||||||||||||
Db        241 MNQCLVATGTHE 252


RESULT 3
JN0561
urokinase-type plasminogen activator receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: JN0561; I46977
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and induc
A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0561
A;Molecule type: mRNA
A;Residues: 1-330 <KRA>
A;Cross-references: UNIPROT:Q05588; UNIPARC:UPI0000137CC6; GB:L03545; NID:g163802; PIDN:
R;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U.
Thromb. Res. 72, 59-70, 1993
A;Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen activator r
A;Reference number: I46977; MUID:94167671; PMID:8122188
A;Accession: I46977
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <REU>
A;Cross-references: UNIPARC:UPI0000137CC6; GB:S70635; NID:g545770; PIDN:AAB30120.1; PID:
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-300/Product: urokinase-type plasminogen activator receptor #status predicted <MAT>
F;21-104/Domain: Ly-6 homology <LY6A>
F;113-201/Domain: Ly-6 homology <LY6B>
F;209-296/Domain: Ly-6 homology <LY6C>
F;301-330/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:48:28 ; Search time 69.715 Seconds
(without alignments)
2934.852 Million cell updates/sec

Title: US-10-679-951-6
Perfect score: 1602
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1568.5	97.9	335	1	UPAR_HUMAN	Q03405 homo sapien
2	1558.5	97.3	335	1	UPAR_PANTR	Q9gk80 pan troglod
3	1504.5	93.9	335	1	UPAR_MACFA	Q9gk78 macaca fasc
4	1501.5	93.7	335	1	UPAR_CERAE	Q9gk79 cercopithec
5	1385.5	86.5	301	2	Q9BWT0_HUMAN	Q9bwt0 homo sapien
6	1235	77.1	336	2	Q9GK77_AOTTR	Q9gk77 aotus trivi
7	1106.5	69.1	281	2	Q6IB52_HUMAN	Q6ib52 homo sapien
8	1101.5	68.8	251	2	Q9UPI5_HUMAN	Q9upi5 homo sapien
9	938	58.6	330	1	UPAR_BOVIN	Q05588 bos taurus
10	896	55.9	322	2	Q9R119_CRIGR	Q9r119 cricetulus
11	890	55.6	328	2	O35771_RAT	O35771 rattus norv
12	879.5	54.9	327	1	UPAR_MOUSE	P35456 mus musculu
13	879.5	54.9	327	2	Q545X5_MOUSE	Q545x5 mus musculu
14	827	51.6	328	1	UPAR_RAT	P49616 rattus norv
15	507	31.6	204	2	Q9TVA9_BOVIN	Q9tva9 bos taurus
16	495.5	30.9	222	1	UPAS_MOUSE	P35457 mus musculu
17	495.5	30.9	222	2	Q91Z14_MOUSE	Q91z14 mus musculu
18	494.5	30.9	220	1	UPAS_RAT	P51573 rattus norv
19	256.5	16.0	88	2	Q9N124_HORSE	Q9n124 equus cabal
20	160	10.0	39	2	Q4RCT4_TETNG	Q4rct4 tetraodon n
21	143.5	9.0	217	2	Q566G7_XENLA	Q566g7 xenopus lae
22	143.5	9.0	2931	2	Q9W2C6_DROME	Q9w2c6 drosophila
23	143.5	9.0	2968	2	Q8MLU9_DROME	Q8mlu9 drosophila
24	141	8.8	199	2	Q4FAD9_9SALA	Q4fad9 desmognathu
25	139	8.7	196	2	Q4FAD0_9SALA	Q4fad0 aneides fer
26	138	8.6	200	2	Q78CF9_NOTAT	Q78cf9 notechis at
27	138	8.6	200	2	Q9PRF7_9SAUR	Q9prf7 notechis sc
28	137.5	8.6	1185	2	Q5EE45_XENLA	Q5ee45 xenopus lae
29	136	8.5	196	2	Q4FAD1_9SALA	Q4fad1 aneides fer
30	136	8.5	199	2	Q4FAD7_9SALA	Q4fad7 desmognathu
31	135	8.4	199	2	Q4FAD6_9SALA	Q4fad6 desmognathu
32	135	8.4	205	2	Q4FAG7_PLEJO	Q4fag7 plethodon j
33	135	8.4	205	2	Q4FAG5_9SALA	Q4fag5 plethodon s
34	135	8.4	205	2	Q4FAG4_9SALA	Q4fag4 plethodon m
35	135	8.4	205	2	Q4FAG6_9SALA	Q4fag6 plethodon c
36	134	8.4	205	2	Q4FAH4_9SALA	Q4fah4 plethodon t
37	134	8.4	205	2	Q4FAH3_9SALA	Q4fah3 plethodon m
38	133	8.3	199	2	Q4FAD3_9SALA	Q4fad3 desmognathu
39	132.5	8.3	201	2	Q9PTC7_OXYMI	Q9ptc7 oxyuranus m
40	132	8.2	199	2	Q4FAE1_9SALA	Q4fae1 plethodon s
41	131	8.2	205	2	Q4FAH1_9SALA	Q4fah1 plethodon m
42	130.5	8.1	200	2	Q9PTC9_9SAUR	Q9ptc9 oxyuranus s
43	130.5	8.1	1546	2	Q5EE46_XENLA	Q5ee46 xenopus lae
44	129.5	8.1	4856	2	Q61EJ2_CAEBR	Q61ej2 caenorhabdi
45	129	8.1	199	2	Q4FAG8_9SALA	Q4fag8 plethodon m

ALIGNMENTS

RESULT 1
UPAR_HUMAN
ID UPAR_HUMAN STANDARD; PRT; 335 AA.
AC Q03405; Q12876; Q15845; Q16887; Q9NYC8; Q9UD69; Q9UEA6; Q9UM92;
AC Q9UMV0;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Urokinase plasminogen activator surface receptor precursor (uPAR) (U-
DE PAR) (Monocyte activation antigen Mo3) (CD87 antigen).
GN Name=PLAUR; Synonyms=MO3, UPAR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-33.
RX MEDLINE=90151622; PubMed=1689240;
RA Roldan A.L., Cubellis M.V., Masucci M.T., Behrendt N., Lund L.R.,
RA Danoe K., Appella E., Blasi F.;
RT "Cloning and expression of the receptor for human urokinase
RT plasminogen activator, a central molecule in cell surface, plasmin
RT dependent proteolysis.";
RL EMBO J. 9:467-474(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=92268511; PubMed=1316922;
RA Min H.Y., Semnani R., Mizukami I.F., Watt K., Todd R.F. III, Liu D.Y.;
RT "cDNA for Mo3, a monocyte activation antigen, encodes the human
RT receptor for urokinase plasminogen activator.";
RL J. Immunol. 148:3636-3642(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RX MEDLINE=94178507; PubMed=8131971;
RA Bayraktutan U., Jones P.;
RT "A novel urokinase receptor on monocyte-like macrophage cell line.";
RL Biochem. Soc. Trans. 21:395-395(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX MEDLINE=93314820; PubMed=8392005; DOI=10.1016/0014-5793(93)81763-P;
RA Pyke C., Eriksen J., Solberg H., Schnack Nielsen B., Kristensen P.,
RA Lund L.R., Danoe K.;
RT "An alternatively spliced variant of mRNA for the human receptor for
RT urokinase plasminogen activator.";
RL FEBS Lett. 326:69-74(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 3).
RC TISSUE=Placenta;
RX MEDLINE=94325556; PubMed=8049431;
RA Casey J.R., Petranka J.G., Kottra J., Fleenor D.E., Rosse W.F.;
RT "The structure of the urokinase-type plasminogen activator receptor
RT gene.";
RL Blood 84:1151-1156(1994).

RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLY-55; ALA-86;
RP GLN-105; ARG-220; LYS-281 AND PRO-317.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP NUCLEOTIDE SEQUENCE OF 1-322 (ISOFORM 1).
RC TISSUE=Lung cancer;
RA Zhu F., Jia S., He F.;
RT "Molecular cloning of UPAR from a human giant cell lung cancer cell
RT line.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE OF 1-18.
RX MEDLINE=95329719; PubMed=7605992;
RA Soravia E., Grebe A., De Luca P., Helin K., Suh T.T., Degen J.L.,
RA Blasi F.;
RT "A conserved TATA-less proximal promoter drives basal transcription
RT from the urokinase-type plasminogen activator receptor gene.";
RL Blood 86:624-635(1995).
RN [11]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=90202929; PubMed=2156852;
RA Behrendt N., Roenne E., Ploug M., Petri T., Loeber D., Nielsen L.S.,
RA Schleuning W.-D., Blasi F., Appella E., Danoe K.;
RT "The human receptor for urokinase plasminogen activator. NH2-terminal
RT amino acid sequence and glycosylation variants.";
RL J. Biol. Chem. 265:6453-6460(1990).
RN [12]
RP PROTEIN SEQUENCE OF 106-116, AND CLEAVAGE BY U-PA.
RX MEDLINE=97182578; PubMed=9030717;
RA Hoeyer-Hansen G., Ploug M., Behrendt N., Roenne E., Danoe K.;
RT "Cell-surface acceleration of urokinase-catalyzed receptor cleavage.";
RL Eur. J. Biochem. 243:21-26(1997).
RN [13]
RP DISULFIDE BONDS, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=93352546; PubMed=8394346;
RA Ploug M., Kjalke M., Roenne E., Weidle U., Hoeyer-Hansen G., Danoe K.;
RT "Localization of the disulfide bonds in the NH2-terminal domain of the
RT cellular receptor for human urokinase-type plasminogen activator. A
RT domain structure belonging to a novel superfamily of glycolipid-
RT anchored membrane proteins.";
RL J. Biol. Chem. 268:17539-17546(1993).
CC -!- FUNCTION: Acts as a receptor for urokinase plasminogen activator.
CC Plays a role in localizing and promoting plasmin formation.
CC Mediates the proteolysis-independent signal transduction
CC activation effects of U-PA. It is subject to negative-feedback
CC regulation by U-PA which cleaves it into an inactive form.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (isoform 1). Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=uPAR1, GPI-anchored;
CC IsoId=Q03405-1; Sequence=Displayed;
CC Name=2; Synonyms=uPAR2, Secreted;
CC IsoId=Q03405-2; Sequence=VSP_006715;
CC Name=3;
CC IsoId=Q03405-3; Sequence=VSP_006714;
CC -!- SIMILARITY: Contains 3 UPAR/Ly6 domains.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR EMBL; X51675; CAA35981.1; -; mRNA.
DR EMBL; M83246; AAA59862.1; -; mRNA.
DR EMBL; X74039; CAA52191.1; -; mRNA.
DR EMBL; U09346; AAA17979.1; -; Unassigned_DNA.
DR EMBL; U09347; AAA17978.1; -; mRNA.
DR EMBL; U09937; AAB60690.1; -; Genomic_DNA.
DR EMBL; U09931; AAB60690.1; JOINED; Genomic_DNA.
DR EMBL; U09932; AAB60690.1; JOINED; Genomic_DNA.
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DR EMBL; AY194849; AAN86351.1; -; Genomic_DNA.
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DR EMBL; AC006953; AAD17388.1; -; Genomic_DNA.
DR EMBL; AC006953; AAD17387.1; -; Genomic_DNA.
DR EMBL; BC002788; AAH02788.1; -; mRNA.
DR EMBL; AF257789; AAF71751.1; -; mRNA.
DR EMBL; S78532; AAD14289.1; -; Genomic_DNA.
DR EMBL; A18757; CAA01421.1; -; Unassigned_RNA.
DR PIR; I52614; I52614.
DR PIR; S39495; S39495.
DR Ensembl; ENSG00000011422; Homo sapiens.
DR HGNC; HGNC:9053; PLAUR.
DR H-InvDB; HIX0015192; -.
DR Reactome; Q03405; -.
DR MIM; 173391; -.
DR GO; GO:0009986; C:cell surface; IEP.
DR GO; GO:0019898; C:extrinsic to membrane; TAS.

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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:13 ; Search time 21.202 Seconds
(without alignments)
1130.835 Million cell updates/sec

Title: US-10-679-951-6
Perfect score: 1602
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1568.5	97.9	335	1	US-08-085-122-13	Sequence 13, Appl
2	1568.5	97.9	335	2	US-08-442-108B-23	Sequence 23, Appl
3	1568.5	97.9	335	2	US-09-949-002-346	Sequence 346, App
4	1568.5	97.9	417	2	US-09-949-002-527	Sequence 527, App
5	515	32.1	90	1	US-08-085-122-5	Sequence 5, Appli
6	515	32.1	90	1	US-08-319-052-5	Sequence 5, Appli
7	515	32.1	90	2	US-08-442-108B-5	Sequence 5, Appli
8	493	30.8	92	1	US-08-085-122-3	Sequence 3, Appli
9	493	30.8	92	1	US-08-319-052-3	Sequence 3, Appli
10	493	30.8	92	2	US-08-442-108B-3	Sequence 3, Appli
11	263.5	16.4	99	1	US-08-085-122-4	Sequence 4, Appli
12	263.5	16.4	99	1	US-08-319-052-4	Sequence 4, Appli
13	263.5	16.4	99	2	US-08-442-108B-4	Sequence 4, Appli
14	183	11.4	34	1	US-08-085-122-11	Sequence 11, Appl
15	183	11.4	34	1	US-08-319-052-21	Sequence 21, Appl
16	183	11.4	34	2	US-08-442-108B-21	Sequence 21, Appl
17	130.5	8.1	204	1	US-08-652-859-2	Sequence 2, Appli
18	130.5	8.1	204	1	US-08-919-706-2	Sequence 2, Appli
19	130.5	8.1	204	1	US-09-153-751-2	Sequence 2, Appli
20	130.5	8.1	204	2	US-09-886-319A-38	Sequence 38, Appl
21	130.5	8.1	228	2	US-09-886-319A-45	Sequence 45, Appl
22	128	8.0	346	2	US-09-991-181-197	Sequence 197, App
23	128	8.0	346	2	US-09-990-444-197	Sequence 197, App
24	128	8.0	346	2	US-09-997-333-197	Sequence 197, App
25	128	8.0	346	2	US-09-992-598-197	Sequence 197, App
26	127	7.9	30	1	US-08-085-122-2	Sequence 2, Appli
27	127	7.9	30	1	US-08-319-052-2	Sequence 2, Appli
28	127	7.9	30	2	US-08-442-108B-2	Sequence 2, Appli
29	120	7.5	220	2	US-09-844-497-2	Sequence 2, Appli
30	120	7.5	220	2	US-10-404-170-2	Sequence 2, Appli
31	117	7.3	21	2	US-08-657-339A-11	Sequence 11, Appl
32	117	7.3	21	2	US-08-457-694A-11	Sequence 11, Appl
33	116.5	7.3	956	1	US-08-897-443-3	Sequence 3, Appli
34	114	7.1	212	2	US-09-886-319A-37	Sequence 37, Appl
35	113.5	7.1	178	2	US-09-270-767-33027	Sequence 33027, A
36	113.5	7.1	178	2	US-09-270-767-48244	Sequence 48244, A
37	107.5	6.7	735	2	US-09-191-647-9	Sequence 9, Appli
38	107.5	6.7	735	2	US-09-540-245A-9	Sequence 9, Appli
39	107.5	6.7	735	2	US-09-540-153-9	Sequence 9, Appli
40	107.5	6.7	735	2	US-10-289-776-9	Sequence 9, Appli
41	107.5	6.7	2556	1	US-08-185-432-17	Sequence 17, Appl
42	107.5	6.7	2556	2	US-08-899-232-2	Sequence 2, Appli
43	107.5	6.7	2556	2	US-09-121-457-2	Sequence 2, Appli
44	106.5	6.6	627	2	US-10-246-658-4	Sequence 4, Appli
45	106.5	6.6	627	2	US-10-843-131-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-085-122-13
; Sequence 13, Application US/08085122
; Patent No. 5519120
; GENERAL INFORMATION:
; APPLICANT: DANO, Keld
; APPLICANT: RONNE, Ebbe
; APPLICANT: BEHRENDT, Niels
; APPLICANT: ELLIS, Vincent
; APPLICANT: HOYER-HANSON, Gunilla
; APPLICANT: PYKE, Charles
; APPLICANT: BRUENNER, Nils
; TITLE OF INVENTION: ANTIBODIES AGAINST THE UROKINASE
; TITLE OF INVENTION: RECEPTOR AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,122
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DANO=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-085-122-13

Query Match 97.9%; Score 1568.5; DB 1; Length 335;
Best Local Similarity 86.3%; Pred. No. 3.4e-135;
Matches 289; Conservative 1; Mismatches 0; Indels 45; Gaps 1;

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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
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Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEE---------------------- 157
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Qy        158 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 195
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Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 2
US-08-442-108B-23
; Sequence 23, Application US/08442108B
; Patent No. 6248712
;  GENERAL INFORMATION:
;    APPLICANT:  DANO, KELD
;    APPLICANT:  BLASI, FRANCESCO
;    APPLICANT:  ROLDAN, ANN LOURING
;    APPLICANT:  CUBELLIS, MARIA VITTORIA
;    APPLICANT:  MASUCCI, MARIA TERESA
;    APPLICANT:  APPELLA, ETTORE
;    APPLICANT:  SCHLEUNING, WOLF-DIETER
;    APPLICANT:  BEHRENDT, NIELS
;    APPLICANT:  KRISTENSEN, PETER
;    APPLICANT:  POLLANEN, JARI
;    APPLICANT:  SALONEN, EEVA-MARJATTA
;    TITLE OF INVENTION:  UROKINASE-TYPE PLASMINOGEN ACTIVATOR
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,108B
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/319,052
;      FILING DATE:  06-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/824,189
;      FILING DATE:  06-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/DK90/00090
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/374,854
;      FILING DATE:  03-JUL-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/334,613
;      FILING DATE:  07-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  DANO=1D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-442-108B-23

  Query Match            97.9%;  Score 1568.5;  DB 2;  Length 335;
  Best Local Similarity   86.3%;  Pred. No. 3.4e-135;
  Matches  289;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

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Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEE---------------------- 157
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Qy        158 ----------------------VLELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 195
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Db        181 FHNNDTFHFLKCCNTTKCNEGPILELENLPQNGRQCYSCKGNSTHGCSSEETFLIDCRGP 240

Qy        196 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 255
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Db        241 MNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPDLDV 300

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Db        301 QYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 335


RESULT 3
US-09-949-002-346
; Sequence 346, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-346

  Query Match            97.9%;  Score 1568.5;  DB 2;  Length 335;
  Best Local Similarity   86.3%;  Pred. No. 3.4e-135;
  Matches  289;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:50:34 ; Search time 60.3717 Seconds
(without alignments)
2007.073 Million cell updates/sec

Title: US-10-679-951-6
Perfect score: 1602
Sequence: 1 MGHPPLLPLLLLLHTCVPAS.....SLTITLLMTARLWGGTLLWT 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1602	100.0	290	4	US-10-679-951-6	Sequence 6, Appli
2	1587.5	99.1	289	4	US-10-679-951-11	Sequence 11, Appl
3	1571.5	98.1	287	4	US-10-087-192-1806	Sequence 1806, Ap
4	1568.5	97.9	335	4	US-10-193-656-6	Sequence 6, Appli
5	1568.5	97.9	335	4	US-10-177-293-362	Sequence 362, App
6	1568.5	97.9	335	4	US-10-295-027-1327	Sequence 1327, Ap
7	1568.5	97.9	335	4	US-10-429-160-75	Sequence 75, Appl
8	1568.5	97.9	335	4	US-10-679-951-8	Sequence 8, Appli
9	1568.5	97.9	335	5	US-10-783-528-97	Sequence 97, Appl
10	1568.5	97.9	335	5	US-10-723-860-2344	Sequence 2344, Ap
11	1568.5	97.9	335	5	US-10-482-029-160	Sequence 160, App
12	1385.5	86.5	301	4	US-10-755-889-424	Sequence 424, App
13	1293.5	80.7	281	4	US-10-679-951-2	Sequence 2, Appli
14	1293.5	80.7	281	4	US-10-679-951-9	Sequence 9, Appli
15	1281.5	80.0	283	5	US-10-993-007-1	Sequence 1, Appli
16	1268	79.2	236	4	US-10-679-951-4	Sequence 4, Appli
17	1263.5	78.9	235	4	US-10-679-951-10	Sequence 10, Appl
18	879.5	54.9	327	4	US-10-087-192-1803	Sequence 1803, Ap
19	515	32.1	90	3	US-09-755-109-5	Sequence 5, Appli
20	493	30.8	92	3	US-09-755-109-3	Sequence 3, Appli
21	263.5	16.4	99	3	US-09-755-109-4	Sequence 4, Appli
22	183	11.4	34	3	US-09-755-109-21	Sequence 21, Appl
23	179.5	11.2	48	4	US-10-425-115-303053	Sequence 303053,
24	143.5	9.0	2931	6	US-11-097-143-31479	Sequence 31479, A
25	138.5	8.6	88	4	US-10-051-874-158	Sequence 158, App
26	135	8.4	366	5	US-10-450-763-45496	Sequence 45496, A
27	130.5	8.1	204	3	US-09-886-319A-38	Sequence 38, Appl
28	130.5	8.1	204	3	US-09-875-520-2	Sequence 2, Appli
29	130.5	8.1	204	4	US-10-376-564-38	Sequence 38, Appl
30	130.5	8.1	228	3	US-09-886-319A-45	Sequence 45, Appl
31	130.5	8.1	228	4	US-10-376-564-45	Sequence 45, Appl
32	128	8.0	346	3	US-09-989-722-197	Sequence 197, App
33	128	8.0	346	3	US-09-989-723-197	Sequence 197, App
34	128	8.0	346	3	US-09-989-279-197	Sequence 197, App
35	128	8.0	346	3	US-09-989-727-197	Sequence 197, App
36	128	8.0	346	3	US-09-989-731-197	Sequence 197, App
37	128	8.0	346	3	US-09-989-732-197	Sequence 197, App
38	128	8.0	346	3	US-09-991-073-197	Sequence 197, App
39	128	8.0	346	3	US-09-990-442-197	Sequence 197, App
40	128	8.0	346	3	US-09-991-163-197	Sequence 197, App
41	128	8.0	346	3	US-09-993-604-197	Sequence 197, App
42	128	8.0	346	3	US-09-990-456-197	Sequence 197, App
43	128	8.0	346	3	US-09-989-721-197	Sequence 197, App
44	128	8.0	346	3	US-09-992-598-197	Sequence 197, App
45	128	8.0	346	3	US-09-989-293A-197	Sequence 197, App

ALIGNMENTS

RESULT 1
US-10-679-951-6
; Sequence 6, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
; APPLICANT: Luther, Thomas
; APPLICANT: Magdolen, Viktor
; APPLICANT: Schmitt, Manfred
; APPLICANT: Muhlenweg, Bernd
; APPLICANT: Kotzsch, Matthias
; TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
; TITLE OF INVENTION: uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
; TITLE OF INVENTION: and Therapeutic Purposes
; FILE REFERENCE: 2923-571
; CURRENT APPLICATION NUMBER: US/10/679,951
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/EP02/03799
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: DE/101 17 381.4
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-679-951-6

Query Match 100.0%; Score 1602; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 6.8e-130;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
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Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180
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Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180

Qy        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240
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Db        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240

Qy        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
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Db        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290


RESULT 2
US-10-679-951-11
; Sequence 11, Application US/10679951
; Publication No. US20040197863A1
; GENERAL INFORMATION:
;  APPLICANT: Luther, Thomas
;  APPLICANT:  Magdolen, Viktor
;  APPLICANT:  Schmitt, Manfred
;  APPLICANT:  Muhlenweg, Bernd
;  APPLICANT:  Kotzsch, Matthias
;  TITLE OF INVENTION: Production of Polyclonal, Monospecific Antibodies Against the
;  TITLE OF INVENTION:  uPAR Variants del4, del5, and del4+5 and Their Use for Diagnosti
;  TITLE OF INVENTION:  and Therapeutic Purposes
;  FILE REFERENCE: 2923-571
;  CURRENT APPLICATION NUMBER: US/10/679,951
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/03799
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: DE/101 17 381.4
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-679-951-11

  Query Match             99.1%;  Score 1587.5;  DB 4;  Length 289;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-128;
  Matches  289;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
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RESULT 3
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; Sequence 1806, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1806
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-087-192-1806

  Query Match             98.1%;  Score 1571.5;  DB 4;  Length 287;
  Best Local Similarity   99.0%;  Pred. No. 2.9e-127;
  Matches  287;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
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Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120

Qy        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNSTH 180

Qy        181 GCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 240
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        181 GCSSEETFLIDCRGPMNQCLVAT---EPKNQSYMVRGCATASMCQHAHLGDAFSMNHIDV 237

Qy        241 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 290
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Db        238 SCCTKSGCNHPDLDVQYRSGAAPQPGPAHLSLTITLLMTARLWGGTLLWT 287


RESULT 4
US-10-193-656-6
; Sequence 6, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
;  APPLICANT: NY, Tor
;  APPLICANT:  HOLMDAHL, Rikard
;  APPLICANT:  LI, Jinan
;  TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
;  FILE REFERENCE: 3810/1J577-US3
;  CURRENT APPLICATION NUMBER: US/10/193,656
;  CURRENT FILING DATE:  2002-07-10
;  PRIOR APPLICATION NUMBER: US 60/304,461
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/304,490
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/305,182
;  PRIOR FILING DATE: 2001-07-13
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank / Q03405
;   DATABASE ENTRY DATE: 1994-02-01
;   RELEVANT RESIDUES: (1)..(335)
US-10-193-656-6

  Query Match             97.9%;  Score 1568.5;  DB 4;  Length 335;
  Best Local Similarity   86.3%;  Pred. No. 6.3e-127;
  Matches  289;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    1;

Qy          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGHPPLLPLLLLLHTCVPASWGLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEEL 60

Qy         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELVEKSCTHSEKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC 120
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:54:24 ; Search time 5.39033 Seconds
(without alignments)
545.203 Million cell updates/sec

Title: US-10-679-951-6
Perfect score: 1602
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	128	8.0	346	6	US-10-131-826A-432	Sequence 432, App
2	128	8.0	346	6	US-10-967-457-77	Sequence 77, Appl
3	112	7.0	1418	6	US-10-453-372-864	Sequence 864, App
4	112	7.0	1620	6	US-10-055-877-213	Sequence 213, App
5	108	6.7	1574	6	US-10-055-877-211	Sequence 211, App
6	106	6.6	1431	7	US-11-128-059-2	Sequence 2, Appli
7	105.5	6.6	1664	6	US-10-055-877-212	Sequence 212, App
8	105.5	6.6	4655	6	US-10-995-561-556	Sequence 556, App
9	105	6.6	1416	7	US-11-128-059-60	Sequence 60, Appl
10	105	6.6	1494	7	US-11-128-059-78	Sequence 78, Appl
11	105	6.6	2086	7	US-11-128-059-82	Sequence 82, Appl
12	105	6.6	2214	7	US-11-080-991-94	Sequence 94, Appl
13	105	6.6	2313	7	US-11-128-059-80	Sequence 80, Appl
14	105	6.6	2358	7	US-11-128-059-74	Sequence 74, Appl
15	105	6.6	2439	7	US-11-128-059-76	Sequence 76, Appl
16	105	6.6	2458	7	US-11-128-059-94	Sequence 94, Appl
17	105	6.6	2551	6	US-10-453-372-256	Sequence 256, App
18	105	6.6	2551	7	US-11-128-059-96	Sequence 96, Appl
19	104.5	6.5	956	7	US-11-113-424-39	Sequence 39, Appl
20	104.5	6.5	961	7	US-11-113-424-35	Sequence 35, Appl
21	104	6.5	915	6	US-10-131-826A-294	Sequence 294, App
22	103.5	6.5	703	6	US-10-821-234-1412	Sequence 1412, Ap
23	103.5	6.5	2764	6	US-10-995-561-691	Sequence 691, App
24	103.5	6.5	2813	6	US-10-995-561-688	Sequence 688, App
25	103.5	6.5	2919	6	US-10-821-234-1133	Sequence 1133, Ap
26	102.5	6.4	2417	6	US-10-453-372-228	Sequence 228, App
27	101.5	6.3	1798	6	US-10-995-561-1033	Sequence 1033, Ap
28	101.5	6.3	1798	6	US-10-995-561-1034	Sequence 1034, Ap
29	101	6.3	1198	6	US-10-453-372-880	Sequence 880, App
30	101	6.3	1398	6	US-10-055-877-46	Sequence 46, Appl
31	101	6.3	1398	6	US-10-453-372-872	Sequence 872, App
32	101	6.3	1450	6	US-10-055-877-48	Sequence 48, Appl
33	101	6.3	1450	6	US-10-453-372-874	Sequence 874, App
34	101	6.3	1594	6	US-10-453-372-860	Sequence 860, App
35	100	6.2	964	7	US-11-137-465-58	Sequence 58, Appl
36	100	6.2	965	7	US-11-147-047-51	Sequence 51, Appl
37	100	6.2	1403	6	US-10-055-877-52	Sequence 52, Appl
38	100	6.2	1403	6	US-10-453-372-878	Sequence 878, App
39	100	6.2	1404	6	US-10-055-877-44	Sequence 44, Appl
40	100	6.2	1404	6	US-10-453-372-870	Sequence 870, App
41	100	6.2	1547	6	US-10-453-372-886	Sequence 886, App
42	100	6.2	1577	6	US-10-055-877-54	Sequence 54, Appl
43	100	6.2	1577	6	US-10-453-372-882	Sequence 882, App
44	100	6.2	1577	6	US-10-453-372-884	Sequence 884, App
45	100	6.2	1620	6	US-10-453-372-868	Sequence 868, App

ALIGNMENTS

RESULT 1
US-10-131-826A-432
; Sequence 432, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.

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;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 432
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-432

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  Best Local Similarity   23.4%;  Pred. No. 0.00018;
  Matches   68;  Conservative   23;  Mismatches  126;  Indels   74;  Gaps   13;

Qy          9 LLLLLHTCVPASWGLRCMQC--KTNGDC-----RVEECALGQDLCRTTIVRLWEEGEELE 61
              |||||      |   | |  |  | :  |      :  :|| | |:|   :  :     :
Db         20 LLLLLRGGAQA---LECYSCVQKADDGCSPNKMKTVKCAPGVDVCTEAVGAVETIHGQFS 76

Qy         62 LVEKSCTHS--EKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECIS 119
              |  : |       | :| |      |     | :  |  | ||       |      || |:
Db         77 LAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQ--CAQDRCN------AKLNLTSRALD--- 125

Qy        120 CGSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNST 179
                                                 | |       | || :|||| | |
Db        126 --------------------------------PAGNE----SAYPPNGVECYSCVGLSR 148

Qy        180 HGCSSEETFLIDCRGPMNQ----CLVATGTHEPKN--QSYMVRGCATASMC-QHAHLGDA 232
                |       :: |    :      |       |    |   |  ||||      | :    |
Db        149 EACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTVSLPVRGCVQDEFCTRDGVTGPG 208

Qy        233 FSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHLSLTITLLMT 279
              |:::    |||  | ||     :  | |  |      | |   ::  |  :|
Db        209 FTLSG---SCCQGSRCNSDLRNKTYFSPRIPPLVRLPPPEPTTVASTTSVT 256


RESULT 2
US-10-967-457-77
; Sequence 77, Application US/10967457
; Publication No. US20050244931A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF545PCT
;  CURRENT APPLICATION NUMBER: US/10/967,457
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: US/09/833,041
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/229,358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256,931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199,384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-967-457-77

  Query Match             8.0%;  Score 128;  DB 6;  Length 346;
  Best Local Similarity   23.4%;  Pred. No. 0.00018;
  Matches   68;  Conservative   23;  Mismatches  126;  Indels   74;  Gaps   13;

Qy          9 LLLLLHTCVPASWGLRCMQC--KTNGDC-----RVEECALGQDLCRTTIVRLWEEGEELE 61
              |||||      |   | |  |  | :  |      :  :|| | |:|   :  :     :
Db         20 LLLLLRGGAQA---LECYSCVQKADDGCSPNKMKTVKCAPGVDVCTEAVGAVETIHGQFS 76

Qy         62 LVEKSCTHS--EKTNRTLSYRTGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECIS 119
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Qy        120 CGSSDMSCERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCYSCKGNST 179
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Db        126 --------------------------------PAGNE----SAYPPNGVECYSCVGLSR 148

Qy        180 HGCSSEETFLIDCRGPMNQ----CLVATGTHEPKN--QSYMVRGCATASMC-QHAHLGDA 232
                |       :: |    :      |       |    |   |  ||||      | :    |
Db        149 EACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTVSLPVRGCVQDEFCTRDGVTGPG 208

Qy        233 FSMNHIDVSCCTKSGCNHPDLDVQYRSGAAPQ----PGPAHLSLTITLLMT 279
              |:::    |||  | ||     :  | |  |      | |   ::  |  :|
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RESULT 3
US-10-453-372-864
; Sequence 864, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-589 A
;  CURRENT APPLICATION NUMBER: US/10/453,372
;  CURRENT FILING DATE:  2003-06-03
;  PRIOR APPLICATION NUMBER: 09/789390
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 09/823187
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/195792
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 09/839446
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/199476
;  PRIOR FILING DATE: 2000-03-25
;  PRIOR APPLICATION NUMBER: 09/863776
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 60/208263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 09/939398
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/227800
;  PRIOR FILING DATE: 2000-08-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1609
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 864
;   LENGTH: 1418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-453-372-864

  Query Match             7.0%;  Score 112;  DB 6;  Length 1418;
  Best Local Similarity   19.9%;  Pred. No. 0.024;
  Matches   66;  Conservative   24;  Mismatches   91;  Indels  150;  Gaps   17;

Qy         16 CVPASWGLRCM----QCKT-NGDCR-----------------------------VEECAL 41
              | |   | ||       :|:| || |:                           :  |||
Db        153 CPPGFQGPRCQYDVDECRTHNGGCQHRCVNTPGSYLCECKPGFRLHTDSRTCLAINSCAL 212

Qy         42 GQDLC-----RTTIVR----------LWEEGEELELVEK--------SCTHSEKTNRTLS 78
              |   |     : || |           | |:|     | :         || |  :  | |:
Db        213 GNGGCQHHCVQLTITRHRCQCRPGFQLQEDGR--HCVRRSPCANRNGSCMHRCQVVRGLA 270

Qy         79 -------YR---TGLKITSLTEVVCGLDLCNQGNSGRAVTYSRSRYLECISC-GSSDMSC 127
                    |:    |     : |  || |  |                    |::  ||     |
Db        271 RCECHVGYQLAADGKACEDVDECAAGLAQCAHG--------------CLNTQGSFKCVC 315

Qy        128 ERGRHQSLQCRSPEEQCLDVVTHWIQEGEEVLELENLPQNGRQCY--------SCKGNS- 178
                |                                    | :|||||          ||: |:
Db        316 HAG-----------------------------YELGADGRQCYRIEMEIVNSCEANNG 344

Qy        179 --THGCSSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVRGCATASMCQH---------- 226
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Db        345 GCSHGCSHTSA------GPLCTCPRGYELDTDQRTCIDVGDCADSPCCQQVCTNNPGGYE 398
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